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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 19:46:25 ; Search time 132 Seconds
(without alignments)
6180.135 Million cell updates/sec

Title: US-09-970-851-1

Perfect score: 1470

Sequence: 1 atgtctccgattcgtatga.....acaccgactgggggtattga 1470

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:**

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:**

2: /cgn2_6/ptodata/2/ina/5B COMB.seq:**

3: /cgn2_6/ptodata/2/ina/6A COMB.seq:**

4: /cgn2_6/ptodata/2/ina/6B COMB.seq:**

5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:**

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106.6	7.3	1572	4	US-09-354-138-125
2	100.2	6.8	1578	4	US-09-354-138-134
3	98.6	6.7	15894	1	US-08-348-891A-1
4	98.6	6.7	15894	1	US-08-905-817-1
5	69	4.7	15462	3	US-09-073-492-1
6	49.2	3.3	7218	1	US-08-232-463-14
7	37.2	2.5	834	4	US-09-621-976-2574
8	36.4	2.5	68750	3	US-09-335-409-1
9	36.4	2.5	68750	4	US-09-568-102-1
10	36.4	2.5	68750	4	US-09-567-969-1
11	36.4	2.5	68750	4	US-09-568-480-1
12	36.4	2.5	68750	4	US-09-568-486-1
13	36.4	2.5	68750	4	US-09-568-472-1
14	36.4	2.5	68750	4	US-09-567-899-1
15	35.8	2.4	505	4	US-09-621-976-15639
16	32.8	2.2	297	4	US-09-252-991A-12783
17	32.6	2.2	2135	4	US-08-933-711B-17
18	32.4	2.2	248	3	US-09-007-005-32
19	32.4	2.2	248	3	US-09-244-796-32
20	32.4	2.2	277	3	US-09-007-005-3
21	32.4	2.2	277	3	US-09-244-796-3
22	32	2.2	31208	4	US-09-852-067-3
23	31.8	2.2	276	4	US-09-313-294A-3427
24	31.8	2.2	289	3	US-09-007-005-17
25	31.8	2.2	289	3	US-09-244-796-17
26	31.8	2.2	291	4	US-09-313-294A-4473
27	31.8	2.2	324	4	US-09-313-294A-7082

28	31.8	2.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
29	31.8	2.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
30	31.6	2.1	71989	4	US-09-443-501A-2	Sequence 2, Appli
31	31.4	2.1	528	4	US-09-621-976-13023	Sequence 13023, A
32	31.4	2.1	4041	3	US-09-105-537-36	Sequence 36, Appl
33	31.4	2.1	6396	4	US-09-620-312D-226	Sequence 226, App
34	31.4	2.1	36778	3	US-09-105-537-5	Sequence 5, Appli
35	31.2	2.1	500	3	US-09-141-000-2	Sequence 2, Appli
36	31.2	2.1	1599	2	US-08-417-495-3	Sequence 3, Appli
37	31.2	2.1	1599	2	US-08-284-391B-3	Sequence 3, Appli
38	31.2	2.1	1599	3	US-09-218-950-3	Sequence 3, Appli
39	31.2	2.1	1599	5	PCT-US92-01785-3	Sequence 3, Appli
40	31.2	2.1	1599	5	PCT-US95-00454-3	Sequence 3, Appli
41	31.2	2.1	3854	2	US-08-720-484A-1	Sequence 1, Appli
42	31.2	2.1	3854	3	US-08-953-823A-1	Sequence 1, Appli
43	31.2	2.1	3854	4	US-09-398-239-1	Sequence 1, Appli
44	31.2	2.1	3854	4	US-09-560-876A-1	Sequence 1, Appli
45	31	2.1	834	4	US-09-621-976-2574	Sequence 2574, Ap

ALIGNMENTS

RESULT 1

US-09-354-138-125

; Sequence 125, Application US/09354138

; Patent No. 6309647

; GENERAL INFORMATION:

; APPLICANT: Paoletti, Enzo

; APPLICANT: Tartaglia, James

; APPLICANT: Taylor, Jill

; APPLICANT: Gettig, Russell

; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)

; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris & Safford, P.C.

; STREET: 530 Fifth Avenue, 25th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/354,138

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/472,379

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/416,646

; FILING DATE: 05-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/224,657

; FILING DATE: 16-APR-1994

; APPLICATION NUMBER: US 08/073,962

; FILING DATE: 08-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/776,867

; FILING DATE: 23-OCT-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/621,614

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,283

; FILING DATE: 31-AUG-1993

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/713,967
FILING DATE: 11-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,666,056
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2860
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 1572 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-354-138-125

Query Match 7.3%; Score 106.6; DB 4; Length 1572;
Best Local Similarity 46.0%; Pred. No. 5.3e-25;
Matches 361; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

QY	499	TCATCCAGCTCAGGTATGGGTGCTACAGTAGGAGGCCATGCTCATATCAGACAGCA 558
DB	505	TCATCTTGGCTCAAAATTTGGATCTGCTAGCTAAAGCGGTGACTCTCTGATATGCA 564
QY	559	GATGAGTGGAAACAAAGAAATCAATAAGTATCATGTCAGCAGGCGAGATCCAGAAAG 618
DB	565	GCGGACTCGAGATGAGAGGTGGATTAAGTATACCAGCAAGAGCTGTGTCGGAGAA 624
QY	619	TACATCTCCACCTGTATGAGGAGTGCAATTCAACTCACAATCAGACATTTCTTGGA 678
DB	625	TTTGAATGAACAAATCTGGCTTGATATTTGTTAGAAACAGGATTTGTCAGGACCTATCT 684
QY	679	GTCCGCAATTTCTTAGTACGAGCTTAAGAGAGCGCGCAATACGCGAGCTGGAGCTCC 738
DB	685	TTGAGCGGATTCATGTGGCGCTCACTTTGACATCAAGATCCCGAGCAACAGCCT 744
QY	739	AGGTATTACAACCTTAGTGGGATGTAGACTCATACATCAGGAACACCGGACTTACTGCA 798
DB	745	AGAAATGCTGAATGATTTGTATATAGATAACTACATTTGTGAAGCTGGGTTAGCTAGT 804
QY	799	TTCTTCTTACACTCAAAATATGGAATATATACAGACATCAGCCCTAGCAGCTCAGCAGC 858
DB	805	TTTCATCTAATCATCAAGTTTGGCAATGAACTATGATATCCGCTCTGGGTTGCATGAG 864
QY	859	CTCACAGGGGATATCCAAAGATGAAGCAGCTCATCGGTTTATATCGGATGAAGGAGAA 918
DB	865	TTTTCCGGAATTAACAATATGATCCCTCATGATGCTATATCAACAGATGGGTGAA 924
QY	919	AATGCGCGGTACATGATCTGTAGGTGACAGTGATCAGATGAGCTTTGCACCGGTGAG 978
DB	925	ACAGCACCGTACATGGTTTCTTTGAAATCTGTTTCAAAACAAATTTAGTGCAGGCTCC 984
QY	979	TATGACAGCTTTATTTCTTTGCGATGGCATGGCATCAGTCTTAGATAAGAACTGGC 1038
DB	985	TACCCATGCTCTGGAGTTATGATGGGGTTGGTGTGAACTTGAAACTCCATGGGA 1044
QY	1039	AAATACCAATTCGCCAGAGACTTCATGAGCACATCTTCTGGAGACTCGGGGTGGAGTAT 1098
DB	1045	GGGTTAAATTCGGTGCATCTTACTTTGACCCAGCTTACTTCAGATCGGGCAAGAAATG 1104
QY	1099	GCTCAGGCTCAGGGGAGTACATCAACGAAGACATGGCTGCTGAGCTAAACTAACCCCG 1158

DB	1105	GTTAGGATCTGCGGCAAAAGTAGCTCTGCACTTGGCGCGAGCTTGGCATCACCAG 1164
QY	1159	GCAGCAAGAGGGGCTGCGAGCTGCTGCCCAACGAGTGTCTGAGGAACTGGCAGCGTG 1218
DB	1165	GAGGAAGCTCAGCTAGTGTGAGAAATAGCATCCAAAGACAACAGAGGACCGGACATTCGA 1224
QY	1219	GATATTCTCTCAACAAGCGGGGTCTCTCACTGGGCTCAGCGATGGAGGCCCCCGAGCC 1278
DB	1225	GCTACTGCTTACGAATCCCAATCACTTTCTGCACTCGGAAGATCCGAAGTCGCGC 1284
QY	1279	TCTCA 1283
DB	1285	AATCA 1289

RESULT 2

US-09-354-138-134
Sequence 134, Application US/09354138
Patent No. 6309647
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Taylor, Jill
APPLICANT: Gettig, Russell
TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
TITLE OF INVENTION: RECOMBINANTS
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,138
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,379
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/416,646
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,657
FILING DATE: 16-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,962
FILING DATE: 08-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/776,867
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,614
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,283
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/713,967
FILING DATE: 11-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,666,056
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2860
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-354-138-134

Query Match 6.8%; Score 100.2; DB 4; Length 1578;
Best Local Similarity 45.6%; Pred. No. 7.5e-23;
Matches 351; Conservative 0; Mismatches 418; Indels 0; Gaps 0;

QY	500	CTATCCAGGCTCAGGTATGGTACAGTACGGAAGGCCATGCTGCATATGAGACGAG	559
DB	506	CCATCTAGCCCAAAATTTGGTCTTGCTCGCAAGGCGGTACGCCCCGACACGCGAG	565
QY	560	ATGAGTCGGAACAACAAGAAGATCAATAAGTACATGCGAGGAGGAGTCCAGAAGAAT	619
DB	566	CTGATTCGGAGCTAAGAAGGTGGATAAAGTACACCCCAAGAAAGGTTAGTTGGTGAAT	625
QY	620	ACATCTCCACCTGTATGAGGATGCAATTCACTCAATCAGACATCTCTGCGAG	679
DB	626	TTAGATTGGAGAGAAAATGGTTGGATGTTGGAGAAACAGGATTCGCGAGACCTCTCCT	685
QY	680	TCCGCATTTTCTTAGTTAGCGAGCTTAAGAGAGCGCCCAATACGCGAGGTGGAGCTCCA	739
DB	686	TACGCCGATTCATGTCGCTCTAATCTCTGGATATCAAGAGAACACCCGGAACAAACCCA	745
QY	740	CGTATTACAACTTAGTAGGGGATGTAGACTCATACATCAGGAACACCGGACTTACTGCAT	799
DB	746	GGATTGCTGAAATGATATGTGACATTCATATATCGTAGAGCGAGGATTAGCCAGTT	805
QY	800	TCCTCTTACACTCAATATAGAAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCC	859
DB	806	TTATCTCGACTATTAACTTTGGGATAGAACTATGTATCTCTGCTCTTTGGACTGCATGAAT	865
QY	860	TCACAGCGGATATCCAAAAGATGAAGCAGCTCATCGTTTATATCGGATGAAGGGAGAA	919
DB	866	TTGCTGCTGATGTTATCCACTTGAGTCTTGTGTAACCTTTACAGCAATGCGGAGAA	925
QY	920	ATGCGCGGTACATGACATTTGCTAGGTGACAGTGTACAGATGAGCTTTTGACCGGCTGAGT	979
DB	926	CTGCACCCCTACATGGTAACTCTGAGAACTCAATTCAGAACCAAGTTCAGTGCAGGATCAT	985
QY	980	ATGCACAGCTTTATCTTTTGGCATGGCATGGCATCAGTCTTAGATAAAGGAAGTGGCA	1039
DB	986	ACCCTCTGCTCTGAGCTATGCCATGGGATGAGAGTGGAACTTTGAAACCTCCATGGGGG	1045
QY	1040	AATACCAATTCCGACAGACTTTCATGACCATCAATCTTGAGACTCGGGGTGGAGTATG	1099
DB	1046	GTTTGAATTTGGCGGATCTTACTTTGATCAGCAATATTTAGATTAGGCGAAGATGG	1105
QY	1100	CTCAGGCTCAGGGGAGTAGCATCAACGAAGACATGGTGTGCTGAGCTAAACCTAACCCCGG	1159
DB	1106	TAAGGAGTCACTGGAAGGTGAGTCCCAATTTGGCATCTGAACTCGGTATCACTGCGG	1165
QY	1160	CAGCAAGAGGGGCTGCGAGCTGCTGCCAAACGAGTGTCTGAGGAACCTGCGAGCGTGG	1219
DB	1166	AGGATGCAAGGCTTGTTCAGAGATTGCAATGTCATCTACTCTGAGGACAAAGATCAGTAGAG	1225
QY	1220	ATATTCCTACTCAACAGCGGGGCTCTCACTGGGCTCAGCGATGGAGG	1268

DB 1226 CGGTGGACCCAGACAGCCCAAGTATCATTTCTACACGGTGATCAAG 1274

RESULT 3
US-08-348-891A-1
Sequence 1, Application US/08348891A
Patent No. 5654136
GENERAL INFORMATION:
APPLICANT: SASAKI, Keiko
APPLICANT: MORI, Takayuki
APPLICANT: MAKINO, Satoshi
TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
ITS ABSOLUTE IDENTIFICATION
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,891A
FILING DATE: 25-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-293625
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: KP-7501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 108..1682
FEATURE:
NAME/KEY: CDS
LOCATION: 1807..3327
FEATURE:
NAME/KEY: CDS
LOCATION: 3438..4442
FEATURE:
NAME/KEY: CDS
LOCATION: 5458..7107
FEATURE:
NAME/KEY: CDS
LOCATION: 7271..9121
FEATURE:
NAME/KEY: CDS
LOCATION: 9234..15782
US-08-348-891A-1

Query Match 6.7%; Score 98.6; DB 1; Length 15894;

Best Local Similarity 45.5%; Pred. No. 1.1e-21;
Matches 350; Conservative 0; Mismatches 419; Indels 0; Gaps 0;

QY 500 CTATCAGGCTCAGGTATGGGTCAAGTAGCGAAGCCATGACTGCTCATATGAGACAGCAG 559
DB |||||
DB 613 CCATCTAGCCCAAAATTTGGGTCTTGGTCTGCGAAGCGGTTCAGCGCCCGACAGCGCAG 672
QY 560 ATGAGTCGGAAACAAAGAAATCAATAGTATCATGCGAAGCGGAGGTCCAGAGAGT 619
DB |||||
DB 673 CTGATTCGGAGCTAAGAGGTGTAAGTACCCCAAAAGAGGGTAGTTGGTGAAT 732
QY 620 ACATCCTCCACCCTGTATGAGGAGTGCATCAATCAGACATTCCTCTGGCAG 679
DB |||||
DB 733 TTAGATTGGAGAGAAATGGTTGGATGTGCTGAGGACAGGATTCGGAGGACCTCTCT 792
QY 680 TCCGCATTTCTTAGTACGAGCTTAAGAGAGGCGGCAATAGCGGAGGTGGAGCTCA 739
DB |||||
DB 793 TACGCCGATTTCTATGCTGCTTAATCTCTGATATCAAGAGAAACCCCGGAAACAAACCCA 852
QY 740 CGTATTACAACTTAGTGGGATGTAGACTCATATCAGGAAACACCGGACTTACTGCAAT 799
DB |||||
DB 853 GGAATGCTGAATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
QY 800 TCTTCTTACACTCAATATGGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCC 859
DB |||||
DB 913 TTATCCTGACTATTAAATTTGGGATAGAAATCTATGATCTCTCTCTGACTGCATGAAT 972
QY 860 TCACAGGCGATATCCAAAGATGAAGCAGCTCATGCTTATATCGATGAAGGAGAAA 919
DB |||||
DB 973 TTGCTGGTGGTATTCACACTTGAGTCTTGATGAACCTTTACCAGCAAAATGGGGGAAA 1032
QY 920 ATGCCCGGTACATGACATTTGCTAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 979
DB |||||
DB 1033 CTGCACCTTACATGATGTAACCTGGAGAACTCAATTCAGAACAGTTTCAAGTGCAGATCAT 1092
QY 980 ATGCACAGCTTTATTTTTCCTATGGGATGCGATCAGTCTTAGATAAGGAACTGGCA 1039
DB |||||
DB 1093 ACCCTCTGCTCTGGAGTATGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1152
QY 1040 ATACCAATTCGCCAGAGCTTCATGACGACATCTTCTGGAGACTCGGGTGGAGTATG 1099
DB |||||
DB 1153 GTTGAACCTTTGGCGATCTTACTTTGATCCAGCATATTTTAGATTAGGCGCAAGATGG 1212
QY 1100 CTCAGGCTCAGGGGATGATCATCAACGAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1159
DB |||||
DB 1213 TAAGGAGTGCAGTGAAGGTGCTTCCATTTGGCATCTGAACTCGGTATCATCTGCG 1272
QY 1160 CAGCAAGAGGGGCTTGGAGTGTCTGCCAACAGAGTGTCTGAGGAAACTGGCAGCGTG 1219
DB |||||
DB 1273 AGGATGCAAGGCTTGTTCAGAGATTGCAATGATCTACTGAGGACAAAGATCAGTAGAG 1332
QY 1220 ATATTCCTTACTCAACAGCGGGTCTTCACTGGGCTCAGCGATGGAG 1268
DB |||||
DB 1333 CGTTGGAGCCAGACAAAGCCCAAGTATCATTTCTTACAGGGTATCAAG 1381

RESULT 4

US-08-905-817-1
; Sequence 1, Application US/08905817
; Patent No. 5824777
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; NUMBER OF INVENTION: 19
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia

COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/905,817
FILING DATE: 04-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,891
FILING DATE: 25-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-293625
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: KP-7501A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 108..1682
FEATURE:
NAME/KEY: CDS
LOCATION: 1807..3327
FEATURE:
NAME/KEY: CDS
LOCATION: 3438..4442
FEATURE:
NAME/KEY: CDS
LOCATION: 5458..7107
FEATURE:
NAME/KEY: CDS
LOCATION: 7271..9121
FEATURE:
NAME/KEY: CDS
LOCATION: 9234..15782
US-08-905-817-1

Query Match 6.7%; Score 98.6; DB 1; Length 15894;
Best Local Similarity 45.5%; Pred. No. 1.1e-21;
Matches 350; Conservative 0; Mismatches 419; Indels 0; Gaps 0;

QY 500 CTATCAGGCTCAGGTATGGGTCAAGTAGCGAAGCCATGACTGCTCATATGAGACAGCAG 559
DB |||||
DB 613 CCATCTAGCCCAAAATTTGGGTCTTGGTCTGCGAAGCGGTTCAGCGCCCGACAGCGCAG 672
QY 560 ATGAGTCGGAAACAAAGAGAAATCAATAGTATCATGCGAAGCGGAGGTCCAGAGAGT 619
DB |||||
DB 673 CTGATTCGGAGCTAAGAGGTGTAAGTACCCCAAAAGAGGGTAGTTGGTGAAT 732
QY 620 ACATCCTCCACCCTGTATGAGGAGTGCATCAATCAGACATTCCTCTGGCAG 679
DB |||||
DB 733 TTAGATTGGAGAGAAATGGTTGGATGTGCTGAGGACAGGATTCGGAGGACCTCTCT 792
QY 680 TCCGCATTTCTTAGTACGAGCTTAAGAGAGGCGGCAATAGCGGAGGTGGAGAGCTCA 739
DB |||||

Db 793 TAGCGGATTTCATGGTGGCTCTAATCCTGGATATCAAGAGAACACCGGAAACAAACCA 852
Qy 740 CGTATTACAACTTAGTAGGGATGTAGACTCATATCATAGAGAACACCGGACTTACTGCAAT 799
Db 853 GGATTGCTGAAATGATGTGACATTTGATACATATATCGTAGAGGAGGATTTAGCCAGTT 912
Qy 800 TCTTCCTTACACTCAATATGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCC 859
Db 913 TTATCCTGACTATTAAGTTTGGGATAGAACTAATGTATCTGCTCTTGGACTGCATGAAT 972
Qy 860 TCACAGCGCATATCCAAAGATGAAGCAGCTCATGGCTTTATATCGATGATGAAGGGAGAA 919
Db 973 TTGCTGGTGGTATATCCACACTTGAATCTTGTGATGAACCTTTACAGCAAAATGGGGAA 1032
Qy 920 ATGCGCGGTACATGACATTTGCTAGGTGACAGTGAATCAGATGAGCTTTGCAACCGCTGAGT 979
Db 1033 CTGCAACCTTACATGGTAAACCTGGAGAACTCAATTCAGAACAAAGTTTCAAGTGCAGGATCAT 1092
Qy 980 ATGCACAGCTTTATCTTTTGGCATGGCATGGCATGCTTGTAGATAAAGAACTGGCA 1039
Db 1093 ACCCTCTGCTCTGGAGCTATGCGCATGGAGTAGAGTGGAACTTGAATACTCCATGGAG 1152
Qy 1040 AATACCAATTCGCAGAGACTTTCATGAGCAATCAITCTCGAGACTCGGGGTGGAGTATG 1099
Db 1153 GTTGAACCTTGGCCGATCTTACTTTGATCCAGCATATTTTAGATTAGGGCAAGAGATGG 1212
Qy 1100 CTGAGGCTAGGGAGTAGCATCAACGAAGACATGGCTGCTGAGCTTAAACTAACCCCGG 1159
Db 1213 TAAGGAGGTGAGTGGAAAGGTGAGTTTCCACATTTGGCATCTGAACCTGGTATCATCTGCG 1272
Qy 1160 CAGCAAGAGGGCGCTGGCAGCTGCTGCCAACAGAGTGTCTGAGGAACTGGCAGCGTGG 1219
Db 1273 AGGATGAAGCTGTTTTCAGAGATTGCAATGCTACTCTAGAGCAAGATCAGTAGAG 1332
Qy 1220 ATATTCCTACTCAACAGCGGGGCTCTCACTGGGCTCAGCGATGGAGG 1268
Db 1333 CGGTTGGACCCAGCAAGCCCAAGTATCATTTCTACAGGTTGATCAAG 1381

RESULT 5
US-09-73-492-1
; Sequence 1, Application US/09073492
; Patent No. 6248578
; GENERAL INFORMATION:
; APPLICANT: Banerjee, Amiya K.
; APPLICANT: Hoffman, Michael A.
; TITLE OF INVENTION: Infectious Clone for Human Parainfluenza
; TITLE OF INVENTION: Virus Type 3
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold LLP
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: USA
; ZIP: 44114-2688
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,492
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Doherty, Pamela A.
; REGISTRATION NUMBER: 40,591
; REFERENCE/DOCKET NUMBER: 23114/04000
; TELEPHONE: (216)622-8200
; TELEFAX: (216)241-0816
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15462 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-073-492-1

Query Match 4.7%; Score 69; DB 3; Length 15462;
Best Local Similarity 53.5%; Pred. No. 9.5e-12;
Matches 144; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

Qy 762 TGTAGACTCATATACATCAGGAACACCGGACTTACTGCTTCTTCTTACACTCAATATGG 821
Db 885 TGTGTGTAATACATAAGAGATGAGGCTTGTCTTCTTCAATACAAATCAGGTATGG 944
Qy 822 AATTAATATCAACAGACATCAGCCCTAGCACTCAGCAGCTCAGAGGCGATATCCAAAGAT 881
Db 945 AATTGAGCTAGATGGCAGCTTTGACTCTTCTCTCAGACCAGATATCAATAGATT 1004
Qy 882 GAAGCAGCTCATCGCTTTATATCGGATGAAGAGGAGAAATGCGCGGTACATGACATTGCT 941
Db 1005 AAAAGCTCTGATGGAATTTGATTTATCAAGAGGACCAAGCGCTCTTTTATCTGTATCT 1064
Qy 942 AGTGACAGTGTACATGAGCTTTGACCGGCTGAGTATGACAGCTTTATCTTTTTC 1001
Db 1065 CAGAGATCTTATCATGCTTGTGAGTTCGACCCAGGCAACTCTCTGCCATATGGAGTTATGC 1124
Qy 1002 CATGGGATGGCATCATGCTTGTAGATAAAG 1030
Db 1125 AATGGGGTGGCAGTTGTACAAACACAGAG 1153

RESULT 6
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109

TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 3.3%; Score 49.2; DB 1; Length 7218;
Best Local Similarity 7.7%; Pred. No. 2.5e-05;
Matches 33; Conservative 210; Mismatches 183; Indels 0; Gaps 0;

QY 1023 AGATAAGGAAGTGGCAATACCAATCCAGGAGACATTCATGAGACATCATTCGTGAG 1082
DB 1453 AGATAGAGATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1394
QY 1083 ACTCGGAGTGGAGTATGCTCAGGCTCAGGGAGTAGCATCAACGAAGACATGGCTGCTGA 1142
DB 1393 RRR 1334
QY 1143 GCTAAACCTAACCCCGGAGCAAGAGGGCTGCGAGCTGCTGCCAAGAGTGTCTGA 1202
DB 1333 RRR 1274
QY 1203 GGAACTGGCAGCGTGGATATTCCTACTCAACGAGCGGGTCTCACTGGGCTCAGCGA 1262
DB 1273 RRR 1214
QY 1263 TGGAGGCCCGGAGCTCTCAGGCTGGATCGAACAAAGTCGAAGGCAACCATGCGCG 1322
DB 1213 RRR 1154
QY 1323 AGATGGGAGACCAATTTCTGGATTGATGAGACAGTGGCGAAGACATGCGAGAAGC 1382
DB 1153 RRR 1094
QY 1383 GCCAACTCCGACAGACACACCCAGCCAGCCCGGAGCTCCCGGCGCATCACA 1442
DB 1093 RRR 1034
QY 1443 AGATAA 1448
DB 1033 GAATTA 1028

RESULT 7
US-09-621-976-2574
; Sequence 2574, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2574
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 497..826
US-09-621-976-2574

Query Match 2.5%; Score 37.2; DB 4; Length 834;
Best Local Similarity 14.2%; Pred. No. 0.066;

Matches 27; Conservative 90; Mismatches 73; Indels 0; Gaps 0;

QY 55 ATGAGCTACCGAGGGGAGAGAGAGGAGACCTTTAAGAGTTGAGTCCAGTATTC 114
DB 9 AAKWMSGSGRSSTRKSSMGRSGWGSRCSTSRMRSKSYGARRCMRRGKAKCM 68
QY 115 ACTCTTAACAGTACGATCCAGAGATAGATGAATTTTTCGGTATTCCTCGGATT 174
DB 69 SWTGMSCWSTGRMSSWRKRKRSWSWTYKWRGYSWTYRMYRCYSWMMWMSRSCYK 128
QY 175 GCTGTTAGGAGGACGCCAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTGTGC 234
DB 129 SRSRMMWMSGRSMCMYGSARWCWRYCMRYRWTCAKSRMKCMWKKWSGSKCK 188
QY 235 TCCCATTTCTC 244
DB 189 SSMCATGCTC 198

RESULT 8
US-09-335-409-1
; Sequence 1, Application US/09335409
; Patent No. 6121029
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/335,409
; CURRENT FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-335-409-1

Query Match 2.5%; Score 36.4; DB 3; Length 68750;
Best Local Similarity 48.1%; Pred. No. 2.1;
Matches 103; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1125 CGAAGACATGCTGCTGAGCTAAACCTAACCCCGGAGCAAGAGGGGCTCGGAGCTGC 1184
DB 31632 CGAGCAGCGGGCTGACCGTACCCCAACGAGACCCGCCAGCAAGCATTTGCTGCCAGGGCGC 31691
QY 1185 TGCCCAACGAGTGTCTGAGGAAACTGCGAGCGTGGATATTCCTACTCAACAAGCGGGGT 1244
DB 31692 TTTGCGAAGAGGGGTGCTCCGGTCCGACGTTGATTTTGTGGAGTGTCCAGGACAGGGA 31751
QY 1245 CCTCACTGGGCTCAGCGATGAGGCGCCCGGAGCCCTCTCAGGGTGGATCGAACAAAGTCGCA 1304
DB 31752 CGGCGCTGGGCGACCCGATCGAGGTGCGAGGCGCTGAGCGAGGTGTATGGTCCAGGGCGCT 31811
QY 1305 AGGCAACCATGTCGCGAGATGGGAGACCCAA 1338
DB 31812 CCGGGGACCGACCGCTGCTGGGGGCGCGCAA 31845

RESULT 9
US-09-568-102-1
; Sequence 1, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-568-102-1

Query Match 2.5%; Score 36.4; DB 4; Length 68750;
Best Local Similarity 48.1%; Pred. No. 2.1;
Matches 103; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1125 CGAAGCATGGCTGCTGAGCTAAACTAACCCCGGAGCAGAGGGGCTGCAGCTGC 1184
DB 31632 CGAGCAGCGGCTGACCGTACCCAAACGGACCCCGCCAGCAAGCATTTGTCGCGCCGCGC 31691

QY 1185 TGCCCAACAGTGTCTGAGAAACTGCGAGGTGGATATTCCTACTCAACAAGCCGGGT 1244
DB 31692 TTTCGCAAGCAGCGGTGCTCCCGTGCAGCTTGAATTTGTGGAGTGTACGGACAGGGA 31751

QY 1245 CTTCACTGGGCTCAGCGATCGAGGCCCCCGAGGCTCTCAGGGTGGATCGAACAAGTCGCA 1304
DB 31752 CGCGCTGGCGCGACCGATCGAGTGCAGCGCTGAGCGAGGTGTATGTTCCAGGGCGCT 31811

QY 1305 AGGGCAACAGATGCCGAGATGGGAGACCCAA 1338
DB 31812 CCGGGGACCGACCGCTGCTGGGGCGCGCCAA 31845

RESULT 10
US-09-567-969-1
Sequence 1, Application US/09567969
Patent No. 6355457
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-567-969-1

Query Match 2.5%; Score 36.4; DB 4; Length 68750;
Best Local Similarity 48.1%; Pred. No. 2.1;
Matches 103; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1125 CGAAGCATGGCTGCTGAGCTAAACTAACCCCGGAGCAGAGGGGCTGCAGCTGC 1184
DB 31632 CGAGCAGCGGCTGACCGTACCCAAACGGACCCCGCCAGCAAGCATTTGTCGCGCCGCGC 31691

QY 1185 TGCCCAACAGTGTCTGAGAAACTGCGAGGTGGATATTCCTACTCAACAAGCCGGGT 1244
DB 31692 TTTCGCAAGCAGCGGTGCTCCCGTGCAGCTTGAATTTGTGGAGTGTACGGACAGGGA 31751

QY 1245 CTTCACTGGGCTCAGCGATCGAGGCCCCCGAGGCTCTCAGGGTGGATCGAACAAGTCGCA 1304
DB 31752 CGCGCTGGCGCGACCGATCGAGTGCAGCGCTGAGCGAGGTGTATGTTCCAGGGCGCT 31811

QY 1305 AGGGCAACAGATGCCGAGATGGGAGACCCAA 1338
DB 31812 CCGGGGACCGACCGCTGCTGGGGCGCGCCAA 31845

RESULT 11
US-09-568-480-1
Sequence 1, Application US/09568480
Patent No. 6355458
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-568-480-1

Query Match 2.5%; Score 36.4; DB 4; Length 68750;
Best Local Similarity 48.1%; Pred. No. 2.1;
Matches 103; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1125 CGAAGCATGGCTGCTGAGCTAAACTAACCCCGGAGCAGAGGGGCTGCAGCTGC 1184
DB 31632 CGAGCAGCGGCTGACCGTACCCAAACGGACCCCGCCAGCAAGCATTTGTCGCGCCGCGC 31691

QY 1185 TGCCCAACAGTGTCTGAGAAACTGCGAGGTGGATATTCCTACTCAACAAGCCGGGT 1244
DB 31692 TTTCGCAAGCAGCGGTGCTCCCGTGCAGCTTGAATTTGTGGAGTGTACGGACAGGGA 31751

QY 1245 CTTCACTGGGCTCAGCGATCGAGGCCCCCGAGGCTCTCAGGGTGGATCGAACAAGTCGCA 1304
DB 31752 CGCGCTGGCGCGACCGATCGAGTGCAGCGCTGAGCGAGGTGTATGTTCCAGGGCGCT 31811

QY 1305 AGGGCAACAGATGCCGAGATGGGAGACCCAA 1338
DB 31812 CCGGGGACCGACCGCTGCTGGGGCGCGCCAA 31845

RESULT 12
US-09-568-486-1
Sequence 1, Application US/09568486
Patent No. 6355459
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30

Db 238 WRARGGKRRAGKSSMMRSMRMSAGKARMCRRMMSCREMSYSOMGSKCMSCRGTC 179
QY 1292 CGAACAAAGTCGCAAGGGCAACCAAGATGCCGAGATGGGGAGACCCCAATTCTTGATTTGA 1351
Db 178 AKWRYARYAKRYASSMGKYMGCRCWCYAKCARMYGYRSTRSRSTGSRGMKYRRRKMYM 119
QY 1352 TGAGAGCAGTGGCGAACAGCATGGGAGAGCGGCAAACTCCGCACAGAGCACCACCCACC 1411
Db 118 WKYMMWSWVCYRMGAAMYGMSARAYRYASMSACKMCSRMMKMMWSMWSMMRCWRSRYRCW 59
QY 1412 CGGAACCCCCCCC 1424
Db 58 MSGKWCYSCCGYC 46

Search completed: September 4, 2004, 00:24:42
Job time : 139 secs

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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 18:08:25 ; Search time 862 Seconds
(without alignments)
7244.607 Million cell updates/sec

Title: US-09-970-851-1
Perfect score: 1470
Sequence: 1 atgtcttcgattcgtatga.....acaccgactgggggtattga 1470

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1161.2	79.0	1747	4 AAC90470	NDV strai
2	1156.4	78.7	1801	6 ABK86576	Newcastle
3	1148.4	78.1	15186	3 AAZ44617	Newcastle
4	1176.2	12.0	1885	2 AAQ14560	Human par
5	166	11.3	15384	4 AAF55095	Nucleotid
6	166	11.3	15384	4 AAF55096	Nucleotid
7	161.2	11.0	15384	4 AAF55097	Nucleotid
8	159.6	10.9	15246	7 ABT13955	Human Cry
9	152	10.3	1527	7 ABT13956	Human Cry
10	152	10.3	15246	7 ABT13954	Morbilliv
11	109.2	7.4	1736	3 AAZ46837	Canine di
12	106.6	7.3	1572	6 ABT198955	Canine di
13	106.6	7.3	15690	6 ABK15038	Canine di
14	106.6	7.3	15690	6 ABK15039	Canine di
15	106.6	7.2	18826	6 ABK15039	Canine di
16	105.6	7.0	1683	2 AAQ70424	Sequence
17	103.4	7.0	1683	2 AAQ70424	Sequence
18	101.8	6.9	1684	2 AAQ54673	Rinder-pe
19	101.8	6.9	15894	2 AAV18270	Measles v
20	101.8	6.9	15894	2 AAV18265	Measles v
21	101.8	6.9	15894	2 AAV18265	Measles v
22	101.8	6.9	15894	2 AAZ22307	Nucleotid
23	101.8	6.9	15894	2 AAZ22302	Nucleotid
24	100.2	6.8	1578	6 ABT198964	Measles v

24	100.2	6.8	15894	2 AAV18271	Measles v
25	100.2	6.8	15894	2 AAV18268	Measles v
26	100.2	6.8	15894	2 AAV18269	Measles v
27	100.2	6.8	15894	2 AAV18264	Measles v
28	100.2	6.8	15894	2 AAZ22301	Nucleotid
29	100.2	6.8	15894	2 AAZ22308	Nucleotid
30	100.2	6.8	15894	2 AAZ22305	Nucleotid
31	100.2	6.8	15894	2 AAZ22306	Nucleotid
32	98.6	6.7	15894	2 AAQ40480	Attenuate
33	98.6	6.7	15894	2 AAV18266	Measles v
34	98.6	6.7	15894	2 AAZ22303	Nucleotid
35	97	6.6	15893	2 AAZ22304	Nucleotid
36	97	6.6	15894	2 AAV18267	Measles v
37	76	5.2	15456	4 AAC85008	Nucleotid
38	76	5.2	15456	6 AAD27765	Bovine pa
39	74.4	5.1	15456	4 AAC85009	Nucleotid
40	74.4	5.1	15456	6 AAD27766	Bovine pa
41	73.2	5.0	15600	7 ACF03818	Human par
42	72.6	4.9	15462	2 AAV18273	HPV-3 PR
43	72.6	4.9	15462	2 AAV18274	HPV-3 PR
44	72.6	4.9	15462	2 AAV83561	Nucleotid
45	72.2	4.9	6843	2 AAV83538	PCR-gener

ALIGNMENTS

RESULT 1
AAC90470
ID AAC90470 standard; DNA; 1747 BP.
XX
AC AAC90470;
XX
DT 13-MAR-2001 (first entry)
XX
DE NDV strain Beaudette C NP gene.
XX
KW NDV; Newcastle disease virus; NP; nucleoprotein; virucide; vaccine;
KW Beaudette C strain; strain B1; leader region; avian pathogen; ds.
XX
OS Newcastle disease virus.
XX
PN WO200067786-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US006700.
XX
PR 05-MAY-1999; 99US-0132597P.
PR 16-DEC-1999; 99US-0171072P.
XX
XX (UTMA-) UNIV MARYLAND BALTIMORE.
XX
XX Samal SK;
XX
XX WPI; 2001-024828/03.
XX
XX New vaccine for Newcastle disease, for treating or preventing Newcastle
XX disease in avian host, comprising attenuated infection Newcastle disease
XX virus.
XX
XX Claim 11; Page; 50pp; English.
XX
XX The present sequence is claimed in a specification relating to the
XX production of novel Newcastle disease virus (NDV) strains from cDNAs and
XX improved live attenuated Newcastle disease vaccines. The vaccines are
XX useful for preventing or treating Newcastle disease in birds. The
XX recombinant NDV may be used to express proteins of other avian pathogens
XX and can be used as a vaccine vector. The new NDV vaccine, unlike previous
XX NDV vaccines, is less likely to revert back to virulence, more stable,
XX and completely apathogenic. Note: The present sequence is not displayed
XX in the specification but a GenBank number is given

SQ Sequence 1747 BP; 493 A; 467 C; 437 G; 350 T; 0 U; 0 Other;

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Query Match      79.0%; Score 1161.2; DB 4; Length 1747;
Best Local Similarity 86.9%; Pred. NO. 0;
Matches 1277; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

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QY	1	ATGTCCTCCGTAATTCAGATGAATCGAGCAGCTCCTCGCTGCTCAGACTCGGCCCAATGGA	60
Db	67	ATGTCCTCCGTAATTTGACGAGTACGAACAGCTCTCGGGCTCAGACTCGGCCCAATGGA	126
QY	61	GCTCAGGAGGGGAGAGAGAGGAGGACATTTTAAGATTGAGTTCAGTCCAGTATTCACCTCTT	120
Db	127	GCTCATGAGAGAGGGGAAAGGGGAGTACCTTAAAGTAGACGCTCCGGTATTTCACCTCTT	186
QY	121	AACAGTGAAGATCCAGAAGATAGATGAAATTTTGGCGTATTTCTGTCTTCGGATGCTGTT	180
Db	187	AACAGTGATGACCCAGAGATAGTGGAACTTTTCGGTATTTGCGCTCCGGATGCTGTT	246
QY	181	AGCGAGGAGCCCAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTGTGTCCTCCAT	240
Db	247	AGCGAAGATGCCAACAAACCACTCAGGCAAGGTGCTCTCATATCTCTTTATGCTCCAC	306
QY	241	TCTCAAGTCATGAGGAACCAATGTGCCCTGACGGAACACAGATGAGGCTCACTGACT	300
Db	307	TCACAGTCATGAGGAACCAATGTGCCCTGACGGAACACAGATGAGGCTCACTGACT	366
QY	301	GTTCTTGAGATCGATGGTTTTTACCAGCAGCGTGCCTCAGTTCAAACACAGGAGTGGGTG	360
Db	367	GTGCTTGAGATTCATGGCTTTTGGCAACGGTATGCCCCAGTTCACCAATAGGATGGAGTG	426
QY	361	TCGTGAGGAGAGGACACAGAGATTCATGGTATGACAGGCTCTCTCCCTGGGCGTGCAGT	420
Db	427	TCGTGAGGAGAGGACACAGAGATTCGCGGATGATGACAGGCTCTCTCCCTGGGCGTGCAGT	486
QY	421	AACGGTACTCCGTTGCTCACGGCTGGGGTTGAAGATGATGCCACCAAGATATCACTGAT	480
Db	487	AATGCAACCCCGTTGCTCACGCGGGGCGGAAGATGATGCCACCAAGATATCACCGAT	546
QY	481	ACTCTGGAAGAAATCCTGTCTATCCAGGCTCAGGTATGGTCACTAGTACGAAGGCCATG	540
Db	547	ACCCCTGAGAGGATCCTCTCTATCAGGCGCCAGTATGGTCACTAGTACGAAGGCCATG	606
QY	541	ACTGCATATGACACAGCAGATCAGTTCGGGAACACGAAGATCAATAAGTACATGACGAA	600
Db	607	ACTGGTATGACCTGCAATGAGTCAGAAACAGACGAATCAATAAGTATATGACGAA	666
QY	601	GGCAGAGTCCAGAAGGTACATCCTCCACCCCTGTATGCAGAGTGCATTCAACTCACA	660
Db	667	GGCAGGTCCTCAAGAAATACATCCTCTACCCCGTATGCAGGAGCACATCCATCTACG	726
QY	661	ATCAGACATCTCGGAGTCCGATTTTCTTAGTTAGGAGCTTAAAGAGGCGCGAAT	720
Db	727	ATCAGACAGTCTCTTGACGTCGCACTCTTTTGGTTAGCGAGCTCAAGAGGCGCGCAAC	786
QY	721	ACGCGAGTGGGAGCTCCACCGTATTACAACTTAGTAGGGGATGTAGACTCATATCAGG	780
Db	787	ACGCGAGTGGTACTCTACTTATTATTAACCTGTAGGGGAGCTAGACTCATATATCAGG	846
QY	781	AACACCGGACTTACTGCAATTCCTCTPACCTCAACTATGGAATTAATACCAAGACATCA	840
Db	847	AATACCGGGCTTACTGCAATTCCTCTGACACTCAAGTACCGAATCAACACCAAGACATCA	906
QY	841	GCCCTAGCACTCAGCAGCTCAGAGGCGATATCCAAAGATGAGCAGCTCATGGTTTA	900
Db	907	GCCCTTGCACTTAGTAGCCTCTCAGGGGCAATCCAGAAATGAAGCAGCTCATGGTTTG	966
QY	901	TATCGGATGAAGGAGAAAATGCGCGGTACATGACATTTGCTTAGGTGATGACCAAGTG	960
Db	967	TATCGGATGAAGGAGATAATGCGCGGTACATGACATTTGCTTAGGTGATGACCAAGTG	1026
QY	961	AGCTTTGCACCGCTGAGTATGCACAGTTTATTTCTTTGTCATGGGATGGCAATCAGTC	1020
Db	1027	AGCTTTGCGCTCCGAGTATGACAACCTTACTCTTCCTGCGCATGGGTATGGCATCAGTC	1086

Qy	1021	TTGATATAAGGAACTGGCGAAATACCAATTCGCCAGAGACTTTCATGAGCACATCATCTTCGG	1080
Db	1087	CTGATATAAGGTACTGGGAAATACCAATTTGCCAGGACTTTATGAGCACATCATCTTCGG	1146
Qy	1081	AGACTCGGGTGGAGTAGTGTCCAGGCTCAGGGAGTAGCATCAACGAGACATGGCTGCT	1140
Db	1147	AGACTTGGAGTAGAGTAGCTCAGGCTCAGGTAAGTAGCATTAACGAGGATATGGCTGCC	1206
Qy	1141	GAGCTAAAACTAACCCCGGCAGCAAGAAGGGGCTGGCAGTGTCTGCCCAACGAGTGTCT	1200
Db	1207	GAGCTAAAGTTAAACCCCGCAGCAAGAGAGAGGCTTGCAGTGTCTGCCCAACGAGTCTCC	1266
Qy	1201	GAGGAACTGGCAGCGTGGATATCTTACTCAACAGCGGGTCTCATCTGGGCTCAGC	1260
Db	1267	GAGGAGACCGACGACATAGACATGCTTACTCAACAGTCGGAGTCTCATCTGGGCTCAGC	1326
Qy	1261	GATGGAGGCCCCCGAGCCTCTCAGGTGGATCGAAACAGTCCGAAGGGCAACAGATGCC	1320
Db	1327	GAGGGGGTCCCAAGCCCTTCAAGCGGATCGAATAGATCGAAGGGCAACAGAAAGCC	1386
Qy	1321	GGAGATGGGAGACCCAAATCTTTGGATTTGATGAGAGCAGTGGCGAACAGCATCGCGAA	1380
Db	1387	GGGGATGGGAGACCCAAATCTTGGATCTGATGAGAGCGGTAGCAAAATGATGAGGAA	1446
Qy	1381	GCGCCAAATCTCCGCACAGAGCACACCCACCCCGGAACCCCCCGAGTCCCGGGCCATCA	1440
Db	1447	GCGCCAAATCTTGCAAGAGGCATCTCCCAATCGGGGCTCTCCCCAACTCTCTGGGCCATCC	1506
Qy	1441	CAAGATAACGACACCGACTGGGGGTATTGA	1470
Db	1507	CAAGATAACGACACCGACTGGGGGTATTGA	1536

DECLASSIFIED

RESULTS 2	
ABK86576	
ID	ABK86576 standard; cDNA; 1801 BP.
XX	
XX	
AC	ABK86576;
XX	
DT	24-SEP-2002 (first entry)
XX	
DE	Newcastle disease virus nucleoprotein cDNA.
XX	
KW	Nucleoprotein; NP; immunodominant epitope; newcastle disease; poultry;
KW	virucide; ND; vaccine, ovo administration; ss; gene.
XX	
OS	Newcastle disease virus.
XX	
Key	Location/Qualifiers
CDS	122..1588
FT	/*tag= a
FT	/product= "Nucleoprotein"
XX	
XX	
PN	WO200236617-A2.
XX	
PD	10-MAY-2002.
XX	
PF	30-OCT-2001; 2001WO-EP012573.
XX	
PR	02-NOV-2000; 2000EP-00203814.
XX	
PA	(ALKU) AKZO NOBEL NV.
XX	
PI	Mebatsion T, Koolen MJM;
XX	
DR	WPI; 2002-527441/56.
DR	P-PSDB; AAU99172.
XX	
PT	New Newcastle disease virus (NDV) mutant, useful as a vaccine for
PT	protecting poultry (e.g. chicken) against Newcastle disease or as a
PT	marker vaccine to distinguish vaccinated animals from those infected with
PT	naturally occurring NDV.

1201 GAGGAACTGGCAGCGGTGATATTCCTACTCAACAGCCGGGTCTCTACTCGGCTCAGC 1260
 1322 GATGATACAGCAGCATATACATGCTACTCAACAGTCGGAGTCTCTACTCGGCTTAGC 1381
 1261 GATGAGGCCCGGAGCCTCTCAGGTGATCGAACAGTCCGAGGGCAACAGATGCC 1320
 1382 GAGGGGGGTCGCAAGCTCTACAAGCGGATCGAATAGATCGCAGGGCAACAGAGGCC 1441
 1321 GGAGATGGGGAGACCCAAATCTTGGATTTGATGAGAGCAGTGGCCGAAACAGCATGCCAGAA 1380
 1442 GGAGATGGGGAGACCCAAATCTTGGATCTGATCGAGAGCGGTAGCAATAGCATGAGGGAG 1501
 1381 GGGCCAAACTCGGCACAGAGCACACCCACCGGAAACCCCGGACTCCCGGGCCATCA 1440
 1502 GGGCCAAACTCTGCACAGGGCACTCCCAATCGGGGCTCCCGCAACTCTCGGGCCATCC 1561
 1441 CAAGATAACGACACCGACTGGGGGTATTGA 1470
 1562 CAAGATAACGACACCGACTGGGGGTATTGA 1591

RESULT 4

AAQ14560
 ID AAQ14560 standard; cDNA; 1885 BP.

AC AAQ14560;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 24-FEB-1992 (first entry)

XX Human para-influenza type 4A virus nucleocapsid protein gene.

XX Vaccine; antigen; ss.

XX Human parainfluenza virus 4a.

OS JP03236783-A.

PN JP03236783-A.

XX 22-OCT-1991.

XX 26-NOV-1990; 90JP-00317931.

XX 27-DEC-1989; 89JP-00336291.

XX (FUJUG) FUJIKURA CHEM CO LTD.

XX WPI; 1991-351134/48.

XX Human para-influenza 4A virus nucleocapsid protein gene - useful for

PT early diagnosis of human para-influenza 4A virus-infection disease, for

PT raw material of vaccine or antigen.

XX Claim 1; Page 1; 9pp; Japanese.

XX The gene can be used for the early diagnosis of human para-influenza type

CC 4A viral infection. Protein expressed from the gene can be used for the

CC prep. of antigens and vaccines. The sequence was obt. from a cDNA

CC generated from mRNA isolated from monkey kidney cells infected with the

CC virus. The position of the ORF is not given. (Updated on 25-MAR-2003 to

CC correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 1885 BP; 652 A; 394 C; 351 G; 488 T; 0 U; 0 Other;

SQ Query Match 12.0%; Score 176.2; DB 2; Length 1885;

Best Local Similarity 48.0%; Pred. No. 3.7e-44;

Matches 567; Conservative 0; Mismatches 608; Indels 6; Gaps 2;

QY 61 GCTCAGCGGGGAGAGAGAGGAGGACCTTTAAGAGTTGAGTCCAGTATTTACTCTT 120
 DB 94 GGTGATCAACAATTTGTGCAATCTGATCTTTAAAGCAGAAATCCCTGTATTTGACTT 153
 QY 121 AACAGTGCAGTCCAGAGATAGATGGAAATTTTGGGGTATTTCTGTTCTCGGATTTGCTT 180
 DB 154 AATACAAATGATCCACAGCAAAAGATTCACTCTAAATGAATTTTGTCTCCGGCAAGCTGTA 213
 QY 181 AGGAGGAGCGCCAAACAAACCGCTCAGGCAAGGTCTCTCATATCCCTCTGCTGCTCCCAT 240
 DB 214 TCATCATCTGCCAAATTCGGCAATTTAAACAGGGGCAATTAATTAATCTCTGCTCTTACAG 273
 QY 241 TCTCAAGTATCAGAGAACCATGTTGCCCTTTCAGGAGAAAACAGAAATCAGGGTACACTGACT 300
 DB 274 GCCACATCAATGCAGAAATCATCTTATGATTTGCTGCCAGAGCCCAAGATGCTGCTTAGG 333
 QY 301 GTTCTTTGAGATCGATGGTTTTT-----ACAGCAGCGTGCCTCAGTTTCAACAGAGAGTG 355
 DB 334 ATCAITTTGAAGTTGATGCAATAGACCCCGCCAGATTATACATTAATTAATTCAGATCT 393
 QY 356 GGGTGTCTGAGGAGAGAGACAGAGATT-CATGGTGTATAGCAGGGTCTCTCCCTCGGGCG 414
 DB 394 GGTCTCGGATGACATCAAGATCAGAGCTTATAGAGCATTTTCCAGAGATTTGCCTATTAGC 453
 QY 415 TGCAGTAAACGGTACTCCGTTTCGTCAAGGCTGGGGTTGAAGATGATGCACAGAGATATC 474
 DB 454 TTAGCTGATAGGACAGTATTTGTTATCCAGAGATGCAGAACATCAGTATCGGATGATATG 513
 QY 475 ACTGATATCTCGAAAGATTCCTGTCTATCCAGGCTCAGGTATGGGTACAGTAGCGAAG 534
 DB 514 GATACATATCTGAATAGGATATTCAGTGTATTAATACAGGTTTGGATAATGGTGTGTA 573
 QY 535 GCATGATCTCATATGAGCAGCAGATGAGTCCGAAACAAAGAGAAATCAATTAAGTACATG 594
 DB 574 TGCATGACAGCTTATGATCAACCCACTGGATCTGAGATCTGAGAGAGAGATTTAGCCAGTATAG 633
 QY 595 CAGCAAGCGCAGAGTCCAGAGAGAGTACATCTCCACCCCTGTATGACAGAGTGCATTAAC 654
 DB 634 CAGCAGGGTAGATGCTGGAGAGATATCAACTGCAACAGATGCAGAAAAATCATCCAA 693
 QY 655 CTCAATATCAGACATTTCTTGGCAGTCCGATTTTCTTAGTTAGCAGCTTTAAGAGAGGC 714
 DB 694 CTAGTAATAAGAGAGAAAGTATGGTTTATAAGACAATTTCTTGTACAGGAAATTTTAAACAGCT 753
 QY 715 CGCAATACGCGAGTGGGAGCTCCACGTTATTAACAATTTAGTAGGGGATGTAGACTCATAC 774
 DB 754 GATAAGGTAGTGTCTTATACCAAGGTTATATGCCATGTGGGAGACATTTGCAAAATAT 813
 QY 775 ATCAGGAAACCGGACTTACTGCATTTCTCTTACATCAAAATATGGAATTAATACCAAG 834
 DB 814 ATAGCTAATGTGCGAATGAGCGCTTCTTTCTTAGCTTAAAGTTTCGGCTTGGGTAATAGA 873
 QY 835 ACATCAGCCCTAGCAGCTCAGCAGGCTCAGCGGATATCCAAAGATCAAGCAGCTCATG 894
 DB 874 TGGAAACCACTTGTCTTTAGTGTGCAATTTCTCGGTGAACCTAGTTAAACTGAAATCTCTTAG 933
 QY 895 GCTTTATATCGATGAGGAGAAATTCGCGGTACATGACATTTGCTAGGTGACAGTGCAT 954
 DB 934 TCATATATCAGAAAGTTAGGTGACAGATCAAGATCTTTGGCTCTCTTGGAAATCTCTGAA 993
 QY 955 CAGATGAGCTTTGCACCCGGCTGAGTATGACAGCTTTTATTTCTTTGCAATGGGATGGA 1014
 DB 994 CTGATGGAAATTTGCTCCAGCTAAATTTACCCACTATTGTTCAGTTATGCTATGGAGTTGGA 1053
 QY 1015 TCAGTCTTTAGATAAGGAACCTGGCAATATACCAATTCGCGAGAGACTTCTATGAGCACATCA 1074
 DB 1054 AGTGTTCAGATCCGCTGATCAGAAATTTATCAGTTTGGAGAGAACTTCTTAAATCCAGT 1113
 QY 1075 TTCTGAGACTCGGGGTGAGTATGCTCAGGCTCAGGGGAGTAGCATCAACGAGACATG 1134
 DB 1114 TACTTCCAGATGTGGTGTGAGACTGCAATGAAACATCAAGGACAGTGTGATCTTAATTT 1173
 QY 1135 GCTGCTGAGCTAAAAACTAAACCCCGCAGCAAGAGGGGCT 1175

Db 1174 GCCTCAGAACTTGAATACTGATGAACAGAGTGGACAT 1214
 AAF55095
 RESULT 5
 ID AAF55095 standard; DNA; 15384 BP.
 XX AAF55095;
 AC AAF55095;
 XX 15-MAY-2001 (first entry)
 XX Nucleotide sequence of a Mumps virus genome.
 DE Encapsidation protein; transcription protein; replication protein;
 KW cell targeting; gene therapy; attenuated virus; vaccine; mumps; ss.
 XX Mumps virus.
 OS WO200109309-A2.
 PN 08-FEB-2001.
 PD 02-AUG-2000; 2000WO-US021192.
 PF 02-AUG-1999; 99US-0146664P.
 PR 23-JUN-2000; 2000US-0213654P.
 PA (AMHP) AMERICAN HOME PROD CORP.
 PI Clarke DK, Johnson EJ, Sidhu MS, Udem SA;
 XX WPI; 2001-123320/13.
 DR Producing a recombinant mumps virus (MUV), useful as a mumps vaccine, by
 PT transfecting or transforming a host cell with a transcription vector
 PT comprising a MUV genome or antigenome, and an expression vector encoding
 PT trans-acting proteins.
 XX Claim 21; Page 95-100; 133pp; English.
 PS The present sequence represents a Mumps virus genome. The specification
 CC describes a method for producing a recombinant mumps virus. The method
 CC comprises transfecting or transforming, in a rescue composition media, a
 CC host cell with a transcription vector comprising a genome or antigenome
 CC of mumps virus, and an expression vector encoding trans-acting proteins
 CC (NP, P and L) necessary for encapsidation, transcription and replication.
 CC The method is carried out under conditions sufficient to permit the co-
 CC expression of the vectors and the production of the recombinant virus.
 CC The recombinant virus has an ability to induce long-lasting immunity with
 CC a single dose and a relatively low level of genome recombination. The
 CC recombinantly produced Mumps viruses are useful in antibody generation,
 CC diagnostic, prophylactic and therapeutic applications, cell targeting,
 CC gene therapy, mutant virus preparation and immunogenic composition
 CC preparation. The method may also produce an attenuated virus for use as a
 CC vaccine for preventing or ameliorating mumps infection
 XX Sequence 15384 BP; 4758 A; 3356 C; 3136 G; 4134 T; 0 U; 0 Other;
 SQ
 Query Match 11.3%; Score 166; DB 4; Length 15384;
 Best Local Similarity 47.5%; Pred. No. 2.1e-40;
 Matches 558; Conservative 0; Mismatches 610; Indels 6; Gaps 2;
 QY 1 ATGCTTCCGTATTCGATGAATACGACAGCTCTCGCTGCTCAGACTCGCCCCCAATGGA 60
 Db 146 ATGTCATCTCTGCTCAGGCAATTTGAGCGGTTTACGATAGAAACAGGAATTCAGACAGG 205
 QY 61 GCTCACCGAGGGGAGAGAGAGGAGGACATTTAGAGTTGAGTCCAGCAATTAATCACTCTT 120
 Db 206 GGTGAGGAGGGTTCAATTCACCGGAGACTTTAAAGTCAGCAGTCAAAGTCTTCGTTATT 265
 QY 121 AACAGTGACATCCAGAAAGATAGATGGAATTTTCGGGTATTTCTGCTTCGGATGCTGTT 180

Db 266 AACACACCCCAATCCACCAACACGCTATCAGATGCTAAACTTTTGTCTTAAGAATAATCTGC 325
 QY 181 AGCGAGAGCGCCAAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTCTGTCTCCCAT 240
 Db 326 AGTCAAAATGCTAGGCGATCTCACAGGCTAGGTGCATTGATAACATTAATTTCTCACTTCCC 385
 QY 241 TCTCAAGTGTAGGAACCATGTTGCCCTTGAGGAAACAGAAATGAGGCTACACTGACT 300
 Db 386 TCAGCAGGCAATGCAAAATCATATTAGATTAGCAGATAGATCACCCGAAAGCTCAGATAGAA 445
 QY 301 GTTCTTTGAGATCGATGGTTTT--ACCAGCAGCGTGCCTCAGTTTCAACAACAGAGTGGGG 358
 Db 446 CGCTGTGAGATTGATGGTTTTTGAGCCTGTGATACATATAGGCTGATTCGAATGACCGGCC 505
 QY 359 TGTCTGAGGAGAGACACAGAGATTCAT----GGTGATAGCAGGGTCTCTCCCTCGGGCG 414
 Db 506 AATCTTACTGCGCAATGAAATGCTGCTATGCTTTGCTTGCAGATGACCTCCCTCCCAACC 565
 QY 415 TGCAGTAAACGCTACTCCGTTTCGTCACGCGTGGGTTGAAGATGATGCCACAGAAATATC 474
 Db 566 ATAAATATGGAACCTCTTACGTACATGAGATGTTGAAGGACAGCCATGTGATGAGATT 625
 QY 475 ACTGATACTCTGGAAGAATCCTGCTATCCAGGCTCAGGTATGGGTCAAGTAGCGAAG 534
 Db 626 GAGCAGTTCTCTGATCGGTGTTACAGTGTACTAATCCAGGCTTGGTATATGTTCTGTAAA 685
 QY 535 GCCATGACTGCTATAGACAGCAGATGAGTCGGAACAAGAAAGATCAATAGTACATG 594
 Db 686 TGTATGACAGCGTACGCCAACCTCGCGGTCTGCTGATCGCGGATTTCCGAAATACCAAG 745
 QY 595 CAGCAAGCAGAGTCCAGAAGAAGTACATCTCCACCTCTGATGAGGAGTGCATTAAC 654
 Db 746 CAGCAAGTCTGCTTGGGCAAGATACATGTCGCAACCGGAGGCCCAAGGTGTGATTCAA 805
 QY 655 CTCACATCAGACATTTCTGCGAGTCCGCAATTTCTTAGTTAGCGAGCTTAAGAGAGCG 714
 Db 806 ACTGCCATCAGGAAAGTCTTGTGTTAGACAGTACCTTACCTCGAATCCAGTTCAGTTGGG 865
 QY 715 CGCATACGCGAGTGGGAGCTCCAGTATTAACAATTTAGTAGGGGATGTAGACTCATAC 774
 Db 866 AGACGGCAGGATTTGCTATCAACACAGATACATGCAATGTTGGTGGTGACATCGAAAGTAC 925
 QY 775 ATCAGGAACACGGACTTTACTGCTTCTCTTCACTCAATATGGAATTAATACCAAG 834
 Db 926 ATTGAGAAATTCAGGCTTACTGCTTCTTCTCACTCTCAATATGCACTAGGGACCAAA 985
 QY 835 ACATCAGCCTTAGCACTCAGCAGCTCAGCGGATATCCAAAGATGAAGCAGCTCATG 894
 Db 986 TGGAGTCTCTATCATTTGGTGCATTACCGGTGAATCCACAGTCCGATCCGTTGATG 1045
 QY 895 CGTTTATCGATGAAGGAGAAATGCGCGGTACATGACATTTGTTAGTGTGACAGTGTAT 954
 Db 1046 ATGTTATCGAGTCTCGGAGAACAAAGCCAGATACCTTGTCTGTTAGAGGCTCCCCAA 1105
 QY 955 CAGATGAGCTTTGACCGGCTGAGTATGTCACAGCTTTTATTCTTTGCTCCATGGGATGCCA 1014
 Db 1106 ATATGAGCTTTGACCCCGGGGCTACCCATTGATATTCAGTTATGCTATGTTAGGAGTCGGT 1165
 QY 1015 TCAGCTTTAGATAAGGAACTGGCAAAATACCAATTCGCCAGAGACTTTCATGAGCAATCA 1074
 Db 1166 ACAGTCTAGATGTTCAATGCGAAATTAACATTTATGACGACCTTTCTTAAACGGTTAT 1225
 QY 1075 TTCTGGAGACTCGGGTGGAGTATGTCAGGCTCAGGGGAGTAGCATCAACGAAGAATG 1134
 Db 1226 TATTTCAAGTTGGGGTTGAGACCGCACGAAGCAACAAAGGCACTGTTGCAACAGAGTA 1285
 QY 1135 GCTGCTGAGCTAAACTTAACCCCGGAGCAAGAA 1168
 Db 1286 GCAGATGATCTGGGCTGACTCTCTGACCAAGAA 1319

RESULT 6
 AAF55096

II	
ID	AAF55096 standard; DNA; 15384 BP.
XX	AAF55096;
AC	AAF55097
XX	15-MAY-2001 (first entry)
DT	Nucleotide sequence of a Mumps virus genome.
XX	
DE	Encapsidation protein; transcription protein; replication protein; cell targeting; gene therapy; attenuated virus; vaccine; mumps; ss.
KW	Mumps virus.
KW	WO200109309-A2.
XX	
OS	08-FEB-2001.
XX	
PN	02-AUG-2000; 2000WO-US021192.
XX	
PF	02-AUG-1999; 99US-0146664P.
XX	
PR	23-JUN-2000; 2000US-0213654P.
XX	
XX	(AMHP) AMERICAN HOME PROD CORP.
PA	
XX	Clarke DK, Johnson EJ, Sidhu MS, Udem SA;
PI	WPI; 2001-123320/13.
XX	
DR	Producing a recombinant mumps virus (MUV), useful as a mumps vaccine, by transfecting or transforming a host cell with a transcription vector comprising a MUV genome or antigenome, and an expression vector encoding trans-acting proteins.
XX	
PT	Claim 21; Page 122-128; 133pp; English.
PT	
PT	The present sequence represents a Mumps virus genome. The specification describes a method for producing a recombinant mumps virus. The method comprises transfecting or transforming, in a rescue composition media, a host cell with a transcription vector comprising a genome or antigenome of mumps virus, and an expression vector encoding trans-acting proteins (NP, P and L) necessary for encapsidation, transcription and replication. The method is carried out under conditions sufficient to permit the co-expression of the vectors and the production of the recombinant virus. The recombinant virus has an ability to induce long-lasting immunity with a single dose and a relatively low level of genome recombination. The recombinantly produced Mumps viruses are useful in antibody generation, diagnostic, prophylactic and therapeutic applications, cell targeting, gene therapy, mutant virus preparation and immunogenic composition preparation. The method may also produce an attenuated virus for use as a vaccine for preventing or ameliorating mumps infection
CC	
CC	Sequence 15384 BP; 4759 A; 3358 C; 3135 G; 4132 T; 0 U; 0 Other;
SQ	
	Query Match 11.3%; Score 166; DB 4; Length 15384;
	Best Local Similarity 47.5%; Pred. No. 2.1e-40;
	Matches 558; Conservative 0; Mismatches 610; Indels 6; Gaps 2;
QY	1 ATGCTTCCTCGTATTCGATGATACGAGCAGCTCTCTCGTGTCTCAGACTCGCCCAATGGA 60
DB	146 ATGTCATCTGTGCTCAAGGCATTTGAGCGGTTACGATAGACGAACTTCAAGACAGG 205
QY	61 GCTCAGCGAGGGGAGAGAGGGAGCAGCTTTAAGAGTTGAGGTCCTCCAGTATTCATCTTT 120
DB	206 GGTGAGGAGGGTTCAATTCACCGGAGACTTTAAAGTCAGCAGTCAAAAGTCTTCGTTATT 265
QY	121 AACAGTACGATCCAGAGATAGATGGAATTTTGGCGGTATTCGTCTTCGGATTGCTGTT 180
DB	266 AACACACCAATCCCAACACAGCTATCATATCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 325
QY	181 AGCAGGAGCCCAACAAACCGCTCAGGCAGGTCCTCATATCCTCTCTCTCTCTCTCTCTCT 240
DB	326 AGTCAAAATGCTAGGGCATCTCACAGGGTAGGTGCAATTGATAACATATTCTCACTTCCC 385
QY	241 TCTCAAGTGATGAGGAACCACTGTTGCCCTTGCGAAGAAACAGAAATGAGCGCTACACTGACT 300
DB	386 TCAGCAGCATGCAAAATCATATTAGATTAGCAGATAGATCACCCGAAAGCTCAGATAGAA 445
QY	301 GTTCTTGAGATCGATGGTTTTT--ACAGCAGCGTGCCTCAGTTCAACAACAGGATGGGG 358
DB	446 CGCTGTGAGATTGATGGTTTTTGGAGCCTGGTACATATAGGCTGATTCCTCAATGACCGGCC 505
QY	359 TGTCTGAGGAGAGACGACAGATTCAT----GGTAGAGAGGGTCTCTCCCTGGGGG 414
DB	506 AATCTTACTGCGCAATGAAATTCGCTATGCTTGTCTTGCTTGAGATGACCTCCCTCCAACC 565
QY	415 TGCAGTAAACGGTACTCCGTTTCGTTCAGCGCTGGGGTTGAAGATGATGACACAGAGATATC 474
DB	566 ATAAATATGGAATCTCTTACGTACATGAGATGTTGAAGGACAGCCATGTGATGAGATT 625
QY	475 ACTGATCTCTGGAAGAAATCCTGTCTATCCAGGCTCAGGTATGGGTACAGTACAGTACG 534
DB	626 GAGCAGTTCTCTGGATCGGTGTTTACAGTGTACTAATCCAGGCTTGGGTAAATGGTCTGTAA 585
QY	535 GCCATGACTGCAATATGAGACAGCAGATGAGTCGGAACAAAGAAAGAAATCAATAAGTACATG 594
DB	686 TGTATGACAGCGTACGCCAACCTGCCGGGTCTGCTGATCGGCGATTTGCGNAATACAG 745
QY	595 CAGCAAGGCAGAGTCCAGGAAGAGTACATCTCCACCCTGTATGCGAGGAGTGCATATCAA 654
DB	746 CAGCAAGGTGCGCTTTCAGGCAAGATACATGCTGCAACCGGAGGCCCAAGGTTGATTCAA 805
QY	655 CTCACATCAGACATTTCTCTGGCAGTCCGATTTCTTTAGTTAGCGAGCTTAAGAGAGGC 714
DB	806 ACTGCCATCAGGAAAAAGTCTTGTGTTAGACAGTACTTTACCTTCGAACTCCAGTTGGCG 865
QY	715 CGCAATACGCGAGTGGGAGCTCCAGGTATTACAACTAGTAGGGGATGTAGACTCATAC 774
DB	866 AGACGCGCAGGATGTTGTTATCAAAACAGATCTATGCAATGTTGGTGCATCGGAAGTAC 925
QY	775 ATCAGGAACACCGGACTTACTGCAATTTCTCTTACACTCAAAATATGGAATTAATACCAAG 834
DB	926 ATTGAGNAATTCAGGCTTACTGCTCTTCTTCTCACTCTCAAAATATGCACTAGGACCCAAA 985
QY	835 ACATCAGCCTTAGCAGCTCAGCAGCCTCAGGGGATATCCAAAGATGAAGCAGCTCATG 894
DB	986 TGGAGTCTCTATCATTTGGGTGCAATTCACCGGTGAACCTCAACAGCTCCGATCCTTGATG 1045
QY	895 CGTTATATCGATGAGGAGGAGAAATGCGCGTACATGACATGCTAGGTGACAGTGAT 954
DB	1046 ATGTTATATCGAGGTCTCGGAGAACAAAGCAGATACCTTGTCTGTAGAGGCTCCCAAA 1105
QY	955 CAGATGAGCTTTGACCGGCTGAGTATGCAAGCTTTTATTCTTTTGGCATGGGATGGCA 1014
DB	1106 ATATGAGCTTTGACCGCGGGGCTACCCATTGATATTCACTTATGCTATGGGAGTCGGT 1165
QY	1015 TCAGTCTTAGATAAAGGAATCGGCAATATCAATTCGCCAGAGACTTTCATGAGCACATCA 1074
DB	1166 ACAGTCTCTAGATGTTCAAAATGCGAAATTTACACTTATGCAACGCTTTCTTAAACGGTTAT 1225
QY	1075 TTCTGGAGACTCGGGGTGGAGTATGCTCAGGCTCAGGGGAGTAGCATCAACGGAAGACATG 1134
DB	1226 TATTTCAGATTTGGGTTGAGCCGCAAGAGACACAGGCACTGTTTGACACAGAGTA 1285
QY	1135 GCTGCTGAGCTTAAACATAACCCCGGAGCAAGAA 1168
DB	1286 GCAGATGATCTGGGCTGACTCTCTGAGCAAGAA 1319
RESULT 7	
AAF55097	
ID	AAF55097 standard; DNA; 15384 BP.
XX	
AC	AAF55097;
XX	
DT	15-MAY-2001 (first entry)
XX	

KW epileptiform disease; multiple sclerosis; chronic fatigue syndrome;
 KW primary lymphadenopathy-associated illness; gene therapy; gene; ds.
 XX Simian parainfluenza virus 5.
 XX WO200277211-A2.
 PN 03-OCT-2002.
 PD 07-FEB-2002; 2002WO-US004117.
 XX 07-FEB-2002; 2001US-0267253P.
 XX 07-FEB-2001; 2001US-0267253P.
 XX (CRYP-) CRYPTIC AFFLICTIONS LLC.
 PA Robbins SJ;
 XX WPI; 2003-040586/03.
 DR New nucleic acid useful for diagnosing and treating idiopathic
 XX neurological disorders, including epileptiform diseases, e.g. epilepsy,
 PT and lymphadenopathy-associated illnesses, and in screening of potential
 PT new antiviral drugs.
 XX Disclosure; Fig 9; 262pp; English.
 PS
 XX The invention relates to an isolated nucleic acid comprising: contiguous
 CC nucleotide positions 1-15246 of a sequence comprising 15246 bp fully
 CC defined in the specification; a nucleotide sequence complementary to the
 CC 15246bp sequence; or a Cryptovirus-specific fragment of the 15246bp or
 CC its complement, at least about 5 nucleotides long. The nucleic acid is
 CC useful in diagnosing and treating many idiopathic neurological,
 CC neurodegenerative, neuropsychological and neuropsychiatric disorders,
 CC including epileptiform diseases (e.g. epilepsy, multiple sclerosis,
 CC chronic fatigue syndrome or subacute sclerosing panencephalitis) and
 CC primary lymphadenopathy-associated illnesses, and in research and
 CC development, including screening of potential new antiviral drugs. The
 CC nucleic acid, protein and the viral particle are useful in manufacturing
 CC a vaccine. The protein is also used in producing a Cryptovirus-specific
 CC antibody. The antibody may also be used in manufacturing a medicament for
 CC the treatment of Cryptovirus infections. The polynucleotides of the
 CC invention can be used to treat disorders by gene therapy. This
 CC polynucleotide sequence represents the coding DNA for the Simian virus 5
 CC protein relating to the invention. (Updated on 27-OCT-2003 to standardise
 CC OS field)
 XX
 SQ Sequence 15246 BP; 4732 A; 3289 C; 3155 G; 4070 T; 0 U; 0 Other;
 Query Match 10.9%; Score 159.6; DB 7; Length 15246;
 Best Local Similarity 47.1%; Pred. No. 2.2e-38;
 Matches 560; Conservative 0; Mismatches 624; Indels 6; Gaps 2;
 QY 1 ATGTCCTCCGTTATTCGATGATACGAGCAGCTCCCTCGCTGCTCAGACTCGCCCAATGGA 60
 DB 152 ATGTCATCCGTCCTTAAGACATATGAGCGATTACGCTCCTCAAGAACTCGAAGATCAG 211
 QY 61 GCTCAGCAGGGGGAGAGAGAGGGAGCACTTTAAGAGTTGAGGTCCTCCAGTATTCTCTT 120
 DB 212 AGTGAGGAGGTACAAATCCCACTACAACACTAAACCGGTAATCAGGATATTATATACTA 271
 QY 121 AACAGTCAGATCCAGAGATAGATGGAATTTTGGGATATCTCTCTTCGGATTCCTGTT 180
 DB 272 ACCTCTAATAACCCAGAGTAAGATCCCGGCTTCTTCTATTCTGCTACGAGATTGTCTC 331
 QY 181 AGCAGAGGAGCCCAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTGCTGCCCAT 240
 DB 332 AGTAATGTTGCAAGGATTTCCCATCGCTTTTGAGACATTAATCAATGTTTTCGTACCA 391
 QY 241 TCTCAAGTATGATGAGGAACCATGTTCCTTTGCGAGAAACAGAAATGAGGCTACATGACT 300
 DB 332 TCAGCCACAAATGCTCAATCATGTCAATTAATAGTGTGACCACTCAGCAAGCTGATATCGAA 451
 QY 301 GTTCTTGATGATCGATGGTTT--ACCAGCAGCGTGCCTCAGTTCAACACAGAGTGGGG 358

DB 452 AGGGTAGAGATCGATGGCTTTGAGGAGGATCATTTCCGCTTAATCCCAATCAAGTTCA 511
 QY 359 TGTCTGAGGAGAGACACAGATTTTCA-----GGTGATAGCAGGGTCTCTCCCTCGGGG 414
 DB 512 GGTATAGCCGTTGGAGAGATCAATGCCTATGCTGCACTTGCAGAGAGNCTACTGCACA 571
 QY 415 TGCAGTAACGGTACTCCGTTTCGTTCACGGCTGGGGTTGAAGATGATGACACCAAGAGATATC 474
 DB 572 CTAAACCATGCAACACCTTTTCGTTGATTCGGAAGTCGAGGAACTGCATGGGATGAGATT 631
 QY 475 ACTGATACTCTCGAAAGAAATCTGCTATCTCAGGCTCAGGTTATGGTTCACAGTAGGGAAG 534
 DB 632 GAGACTTTCTTAGATATGTTTACAGTGTCTTAATGCAGGCATGGATAGTACTTCCAAAG 691
 QY 535 GCATGACTGCATATGAGACAGACAGATGATCGGAAACAGAGAAATCAATAAGTATCATG 594
 DB 692 TGCATGACTGCGCCAGACCAACCTGCTGCTTCTATTGAGAAACGCTGCATAAATATCGT 751
 QY 595 CAGCAAGGAGAGTCCAGAAAGATACATCTCCAGCCTGTATGTCAGGAGTGCATTTCAA 654
 DB 752 CAGCAAGGAGAGTCAACCCGAGATATCTCTGCAACCGAGGCTCGACGATAATATCCAG 811
 QY 655 CTCACAAATCAGACATCTCTGGCAGTCCGCAATTTTCTTAGTAGGAGCTTAAGAGAGGC 714
 DB 812 AATGTAATCCGAAAGGAAATGGTGTGTCAGACATTTTCTCCTTGAACCTGCAGCTTGGC 871
 QY 715 CGCAATAGCGCAGGTGGAGCTCCAGTATTTACAACTTAGTAGGGATGTAGACTCATAC 774
 DB 872 CGAGCACAAGACCTTGTATCAAAATAGGTATTTATGCTATGTTAGGGGATGTTGGAAAGTAT 931
 QY 775 ATCAGGAACACCGGACTTACTGCAATCTCTCTTACACTCAAAATATGGAATTAATACCAAG 834
 DB 932 ATAGAGAAATTTGGAATGGAGGCTTCTTTTTCACACTTAAATATGCAATTAGGAACATAGA 991
 QY 835 ACATCAGCCCTAGCCTCAGCAGCCTCAGGCGATATCCAAAGATGCAAGCAGCTCATG 894
 DB 992 TGGCCCACTTGTCTTAGCTGCACTTTTTCAGGAGAGCTAACAAAGCTAAAGTCCCTCATG 1051
 QY 895 CGTTTATCGGTGAAGGAGAAATGCGCGTACATGACATGCTAGGTGACAGATGAT 954
 DB 1052 GCATTAACAGACACCTTGGTGAGCAGCCCGATTTTGGCCCTATTGGAGTCAACCAT 1111
 QY 955 CAGATGAGCTTTGACACCGGCTGAGTATGCAAGCTTTTATTTCTTTTGGCATGGGATGGCA 1014
 DB 1112 TTGATGATTTTGTGTCAGCAAACTACCCACTGCTATATAGTATGCTATGGGAATAGGC 1171
 QY 1015 TCAGTCTTAGATAAAGGAACTGGCAATATACCAATTCGCCAGAGACTTCATCAGCACATCA 1074
 DB 1172 TATGTTTAGATGTCAACATGAGGAATACGCTTTTCTCCAGATCATATGAACAGACA 1231
 QY 1075 TTCTGGAGACTCGGGTGGAGTATGCTCAGGCTCAGGGGAGTAGCATCAACGAAAGACATG 1134
 DB 1232 TATTTCGAATTTGGGAATGGAATCTGCAAGAAACACACAGGTTGCAAGTATGATGAGGATG 1291
 QY 1135 GCTGCTGAGCTTAAACCTAACCCCGCAGCAGAAAGGGCCCTGGCAGCTGC 1184
 DB 1292 GCAGAGATCTCGGCTTAACCTCAAGCCGACCGCAGATGGCAATATAC 1341

RESULT 9

ABT13956

ID ABT13956 standard; DNA; 1527 BP.

XX ABT13956;

XX AC ABT13956;

XX DT 13-FEB-2003 (first entry)

XX DE Human Cryptovirus strain BBR DNA region SEQ ID No 3.

XX Neuroprotective; virucide; anticonvulsant; antiinflammatory; Cryptovirus;
 KW idiopathic; neurological; neurodegenerative; neuropsychological; vaccine;
 KW epilepsy; neuropsychiatric disorder; subacute sclerosing panencephalitis;

epileptiform disease; multiple sclerosis; chronic fatigue syndrome; primary lymphadenopathy-associated illness; gene therapy; ds.

Rubulavirus sp.

WO200277211-A2.

03-OCT-2002.

07-FEB-2002; 2002WO-US004117.

07-FEB-2001; 2001US-0267253P.

(CRYP-) CRYPTIC AFFLICTIONS LLC.

Robbins SJ;

WPI; 2003-040586/03.

P-PSDB; ABJ18502.

New nucleic acid useful for diagnosing and treating idiopathic neurological disorders, including epileptiform diseases, e.g. epilepsy, and lymphadenopathy-associated illnesses, and in screening of potential new antiviral drugs.

Disclosure; Page 195-197; 262pp; English.

The invention relates to an isolated nucleic acid comprising: contiguous nucleotide positions 1-15246 of a sequence comprising 15246 bp fully defined in the specification; a nucleotide sequence complementary to the 15246bp sequence; or a Cryptovirus-specific fragment of the 15246bp or its complement, at least about 5 nucleotides long. The nucleic acid is useful in diagnosing and treating many idiopathic neurological, neurodegenerative, neuropsychological and neuropsychiatric disorders, including epileptiform diseases (e.g. epilepsy, multiple sclerosis, chronic fatigue syndrome or subacute sclerosing panencephalitis) and developmental, including screening of potential new antiviral drugs. The nucleic acid, protein and the viral particle are useful in manufacturing a vaccine. The protein is also used in producing a Cryptovirus-specific antibody. The antibody may also be used in producing a Cryptovirus-specific treatment of Cryptovirus infections. The polynucleotides of the invention can be used to treat disorders by gene therapy. This polynucleotide sequence represents a DNA region of the human Cryptovirus strain BBR of the invention

Sequence 1527 BP; 451 A; 355 C; 364 G; 357 T; 0 U; 0 Other;

Query Match	10.3%	Score 152;	DB 7;	Length 1527;
Best Local Similarity	46.1%;	Pred. No. 1.4e-36;		
Matches 549;	Conservative 0;	Mismatches 635;	Indels 6;	Gaps 1;
QY	1	ATGCTCTCCGTATTTCGATGTAATGAGACAGCTCTCTCGTCTCAGACTCGCCCAATGGA	60	
Db	1			
QY	61	GCTCAGCGAGGGGAGAGAGAGGGAGGACATTTAAGAGTTTGAGTTCAGGTCCCAAGTATTCACCTTT	120	
Db	61	AGTGAAGAAGGCACATCCCACTCAACACTAAACCGGTATTCAGGGTATTTGTACTA	120	
QY	121	AACAGTGACGATCCAGAGATAGATGAAATTTTGGCGTATTTCTGTCTTCGGATTCGTGTT	180	
Db	121	ACCTCTAATAACCCAGAGCTAAGATCCCGGCTTCTTCTATTCTGCCTACGGATTTGTC	180	
QY	181	ACGAGGAGCGCAACAAACGGCTCAGCGAAGTGCTCTCATATCCCTCTGTGTCGCCAT	240	
Db	181	AGTATGTGCAAGGATTTCCCATCGCTTTGGAGCATTTACTTCAATGTTTTTCGTACCA	240	
QY	241	TCTCAAGTGATGAGGAACCATGTTGCGCTTGCAGGAAACAGAAATGAGGCTACACTGACT	300	
Db	241	TCAGCTACAATGCTCAATCATATGTCAATTAGCTGACCGATCCAGCAAGCTGATATCGAA	300	
QY	301	GTTCTTGATCGATGGTTTTTACCAGACGGTGCCTCAGTTTCAACACAGGAGTGGGGTG	360	

Db	301	AGGGTAGAGATCGATGGCTTTGAGGAGGATCAATTCGGCTTAATTCCTCAATGCTCGCTCA	36
QY	361	TCGTAGGAGAGAGCAGACA-----GATTCATGSGTAGACGAGGCTCTCTCCCTCGGGCG	414
Db	361	GGTATGAGCCGTGGAGAGATCAATGCTATGCTGCACTTGCGAAGAGATCTACTCTGCACA	420
QY	415	TCAGTAAACGGTACTCCGTTGCTGCAGGCTGGGGTTGAAGATGATGCACCAAGATATC	474
Db	421	CTAAACCATGCAACACCTTTGCTGATTCGGAAGTCGAGGNACTGCATGGGACGAGATT	480
QY	475	ACTGATACTCTGGAAAGAACTCTGTCTATCCAGGCTCAGGTATGGGTACAGTAGCGGAAG	534
Db	481	GAGACTTCTTAGATATGTGTTACAGTGTCTTAATGCGAGGCATGATAGTACTTGCACAG	540
QY	535	GCCATGACTGTCATATGACACGACGATGAGTCGGAAACAAGAAGAACTCAATAAGTACATG	594
Db	541	TGCATGACTGCCCAGACCAACCTGCTGCTTCTATTGAGAAACGGCTCGAAAAATATCGT	600
QY	595	CAGCAAGCGAGAGTCCAGAAAGTACATCTCCACCCTGTATGCGAGGAGTGCATTCAA	654
Db	601	CAGCAAGCGAGGATCAACCCCAAGATATCTCTGCAACCGGAGGCTCGACGAATAATCCAG	660
QY	655	CTCAAACTCAGACATTTCTCGCAGTCGGCATTTTCTTAGTTAGCGAGCTTAAGAGAGGC	714
Db	661	AATGTAATCCGGAAGGNAATGCTGTCAGACATTTCTCACTTGAACCTGCGAGTTGCC	720
QY	715	CGCAATACGGCAGGTGGAGGCTCCAGTATTAACAACCTTAGTGGGGATGTAGACTCATAC	774
Db	721	CGAGCAAAAGCCTTGTTATCAAAATAGGTATATGCTATGGTAGGGATTTGGAAAGTAT	780
QY	775	ATCAGGAACACCGGACTTACTGCAATCTCTCTTACACTCAATATGGAATTAATACCAAG	834
Db	781	ATAGAGAAATGTGGAATGGGAGGCTTTTGTGACACTAAATATGATTAGGAACCCAGA	840
QY	835	ACATAGCCCTTAGCACTCAGCAGCCTCAGAGCGGATATCCAAAAGATGAAGCAGCTCATG	894
Db	841	TGGCCACACTTGTCTTAGCTGCAATTTTCAGGAGAGCTAACAAAGCTAAGTCCCTCATG	900
QY	895	CGTTTATATCGGATGAAGGAGGAATAATGCGCCGTACATGACATGCTTAGGTGACAGTGTAT	954
Db	901	GCATTGTACAGACCTTGTGTGAGCGGCCGATATTTGGCCCTATTGGAGTCACCAAC	960
QY	955	CAGATGAGCTTTGCACCGCTGAGTAGTCACAGCTTTATTTCTTTGCGATGGGATGGCA	1014
Db	961	TTGATGGATTTGCTGCAGCAAACTATCCATTGCTATATAGCTATGCTATGGGAATAGGC	1020
QY	1015	TCAGTCTTAGATAAAGAACTGCGAAATACCAATTTGCCAGAGACTTCATGAGCAATCA	1074
Db	1021	TATGTGTAGATGTCAACATGAGGNACTACGCTTTCTCCAGATCATACATGAATAAGACA	1080
QY	1075	TTCTGGAGACTCGGGGTGGAGTAGTGTCTCAGGCTCAGGGAGTAGAGTCAACGAAGACATG	1134
Db	1081	TATTTCCAAATGGGAATGGAACATGCAAGAAACAACAGGTCAGTTGACATGAGGATG	1140
QY	1135	GCTGCTGAGTTAAACTAACCCCGGCAGCAAGAGGGGCTCGCAGCTGC	1184
Db	1141	GCAGAAGATCTCGGTCTAACTCAAGCCGAACCGACCGAGATGCGAAATATC	1190

RESULT 10

ABT13954

ID ABT13954 standard; DNA; 15246 BP.

AC ABT13954:

XX

DT 13-FEB-2003 (first entry)
YY

Human Cryptovirus strain P

XX
XX

KW Neuroprotective; virucide; anticonvulsant; antiinflammatory; Cryptovirus;
KW idionathic; neuroprotective; anticonvulsant; antiinflammatory; Cryptovirus;

KW idiopathic; neurodegenerative; neuropsychological; vaccine;
KW idiopathic; neurodegenerative; neuropsychological;
KW epilepsy; neuropsychiatric disorder; subacute sclerosing

acute sclerosing panencephalitis;

KW	epileptiform disease; multiple sclerosis; chronic fatigue syndrome;	
KW	primary lymphadenopathy-associated illness; gene therapy; gene; ds.	
XX	Rubulavirus sp.	
XX	WO200277211-A2.	
XX	03-OCT-2002.	
XX	07-FEB-2002; 2002WO-US004117.	
XX	07-FEB-2001; 2001US-0267253P.	
XX	(CRYP-) CRYPTIC AFFLICTIONS LLC.	
PA	Robbins SJ;	
XX	WPI; 2003-040586/03.	
DR	New nucleic acid useful for diagnosing and treating idiopathic	
PT	neurological disorders, including epileptiform diseases, e.g. epilepsy,	
PT	and lymphadenopathy-associated illnesses, and in screening of potential	
PT	new antiviral drugs.	
XX	Claim 1; Fig 9; 262pp; English.	
XX	The invention relates to an isolated nucleic acid comprising: contiguous	
CC	nucleotide positions 1-15246 of a sequence comprising 15246 bp fully	
CC	defined in the specification; a nucleotide sequence complementary to the	
CC	15246bp sequence; or a Cryptovirus-specific fragment of the 15246bp or	
CC	its complement, at least about 5 nucleotides long. The nucleic acid is	
CC	useful in diagnosing and treating many idiopathic neurological,	
CC	neurodegenerative, neuropsychological and neuropsychiatric disorders,	
CC	including epileptiform diseases (e.g. epilepsy, multiple sclerosis),	
CC	chronic fatigue syndrome or subacute sclerosing panencephalitis) and	
CC	primary lymphadenopathy-associated illnesses, and in research and	
CC	development, including screening of potential new antiviral drugs. The	
CC	nucleic acid, protein and the viral particle are useful in manufacturing	
CC	a vaccine. The protein is also used in producing a Cryptovirus-specific	
CC	antibody. The antibody may also be used in manufacturing a medicament for	
CC	the treatment of Cryptovirus infections. The polynucleotides of the	
CC	invention can be used to treat disorders by gene therapy. This	
CC	polynucleotide sequence represents the coding DNA for the human	
CC	Cryptovirus strain BBR protein of the invention	
XX	Sequence 15246 BP; 4753 A; 3273 C; 3131 G; 4089 T; 0 U; 0 Other;	
SQ	Query Match 10.3%; Score 152; DB 7; Length 15246;	
	Best Local Similarity 46.1%; Pred. No. 5.4e-36;	
	Matches 549; Conservative 0; Mismatches 635; Indels 6; Gaps 1;	
QY	1 ATGCTTCCTCGATTCGATGAATACGAGCAGCTCCTCGCTGCTCAGACTCGCCCAATGGA 60	
DB	152 ATGTCATCCGTGCTTAAGCATATAGAGATTACACTCACTCAAGAACTCAAGATCAG 211	
QY	61 GCTCAGCAGGGGAGAGAGAGGAGCCTTTAAGATTGAGTTCAGGTCCTGATTTACTCTT 120	
DB	212 AGTGAAGAGGCAATCCCACTACACACTAAACCGGTTATCAGGGTATTTGTACTA 271	
QY	121 AACAGTACGATCAGAGATAGATGATGATTTTCGGTATTCCTGCTCGGATTCGTT 180	
DB	272 ACCTCTAATACCCAGAGCTAAGATTCCTGCTTCCTTCTTCTGCTACGATTTGTTCTC 331	
QY	181 AGCAGGAGCGCAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTGCTGCCAT 240	
DB	332 AGTAATGTGCAAGGATTCCTTCCTTTGGAGCATTTACTACAAATGTTTGGTACCA 391	
QY	241 TCTCAAGTATGAGGAACCATGTTGCTTCCCTTGCAGGAAACAGAAATGAGGCTACACTGACT 300	
DB	392 TCAGCTACATGCTCAATCATGTCAAAATAGTGTGACCAAGTCAACCAAGAGCTGATATCGAA 451	
QY	301 GTTCTTGATGATGGTTTACAGCAGCGCTGCTCAGTTCAACACAGAGGATCGGGTG 360	

DB	452 AGGGTAGAGATCGATGGCTTTTGGAGGGGATCATTCCGCTTAATTCCCAATGCTCGCTCA 511	
QY	361 TCTGAGGAGAGCACAGA-----GATTCATGGTGATAGCAGGGTCTCTCCTCGGGCG 414	
DB	512 GGTATGAGCCGTTGGAGAGATCAATGCCTATGCTGCACTTGCAGAGATCTACTGACACA 571	
QY	415 TGCAGTAACGGTATCTCCGTTTGTTCAGCGCTGGGGTTGAAGATGATGCACCAAGAAATATC 474	
DB	572 CTAACCAATGCAACACCTTTGTTGATTCGAAGTCGAGGGAACCTGCATGGACGAGATT 631	
QY	475 ACTGATATCTCGAAGAAATCTGTCTATCCAGGCTCAGGTATGGTACAGTAGGGAAG 534	
DB	632 GAGACTTTCTTAGATATGTGTTACAGTGTCTTAATGTCAGGCAATGATATGACTTGCAG 691	
QY	535 GCATGATCTGCATATGAGACAGCAGATGATCGGAAACAAAGAAATCAATAAATACATG 594	
DB	692 TGCATGACTGCGCCAGACCAACCTGCTGTTCTTATTTAGAAACGCTGCAGAAATATCGT 751	
QY	595 CAGCAAGGAGAGTCCAGAAAGTAATCATCTCCACCTGTATGAGAGGATGCAATTCAA 654	
DB	752 CAGCAAGGAGAGTCAACCAAGATATCTCTCAACCGAGGCTCGACGAATATCCAG 811	
QY	655 CTCACAAATCAGACATTTCTGTGAGTCCCATTTTCTTAGTTAGTTCAGGAGCTTAAGAGGC 714	
DB	812 AATGTAATCCGGAAGGGAATGGTGTGTCAGACATTTCTCACCCTTTGAACTGCAGCTTGC 871	
QY	715 CGCAATACGGCAGGTGGAGCTCCAGTATTACAACCTTAGTAGGGGATGTAGACTCATAC 774	
DB	872 CGAGCAACAAGCCTTGTATCAATAGTATATGCTATGTTAGGGGATGTGGAAGATAT 931	
QY	775 ATCAGGAACACCGGACTTACTGCAATTTCTCTTACACTCAATATGGAATTAATACCAAG 834	
DB	932 ATAGAGAATTTGGAATGGAGGCTTTCTTTTGACACTAAATATATGCAATTAGGAACCA 991	
QY	835 ACATAGCCTTAGCACTCAGACGCTCAGGCGATATCCAAAGATGAGCAGCTCATG 894	
DB	992 TGCCCAACACTTGTCTTTAGCTGCAATTTTCAGGAGAGCTAACAAAGCTAAAGTCCCTCATG 1051	
QY	895 CGTTTATTCGGATGAAGGGAGAAATGCGCGTACATGACATTTGCTAGGTGACAGTGAT 954	
DB	1052 GCATTTACAGACCCCTTGTGTAGCAGGCCGATATTTGGCCCTATTGGAGTACCACAC 1111	
QY	955 CAGATGAGCTTTGCACCGCTGAGTATGACAGCTTTATTTCTTTTGGCATGGGATGGCA 1014	
DB	1112 TTGATGATTTTGTCTGACCAACTATCCATTCATATAGCTATGCTATGGGAATAGGC 1171	
QY	1015 TCAGTCTTAGATAAAGAACTGGCAATACCAATTCGCTCCAGAGACTTTCATGAGCACATCA 1074	
DB	1172 TATGTTGTAGATGTCAACATGAGGAACCTACGCTTCTCCAGATCANTACATGAATAGACA 1231	
QY	1075 TTCTGGAGACTCGGGTGGAGTATGCTCAGGCTCAGGGGAGTAGCATCAACGAAGACATG 1134	
DB	1232 TATTTCCAAATGGGAATGGAACTGCAAGAAACACAGGGTGCAGTTGATGATGAGGATG 1291	
QY	1135 GCTGCTGAGCTTAAACTAACCCCGGAGCAAGAGGGGCTTGCGAGCTGC 1184	
DB	1292 GCAGAAGATCTCGGTCTAATCTCAAGCCGAGCCGAGATGGCAATATC 1341	
RESULT 11		
AAZ46837		
ID	AAZ46837 standard; cDNA to mRNA; 1736 BP.	
XX	AAZ46837;	
XX	06-AUG-2003 (revised)	
DT	10-APR-2000 (first entry)	
XX	Morbillivirus antigenic protein encoding nucleotide sequence.	
DE	Antigenic; nucleocapsid protein; canine distemper virus; CDV;	
KW	Morbillivirus; Paramyxovirus; ss.	
XX		

OS Canine distemper virus.

PN JP11346768-A.
 PD 21-DEC-1999.
 XX
 PF 03-JUN-1998; 98JP-00155072.
 XX
 PR 03-JUN-1998; 98JP-00155072.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 DR WPI; 2000-109685/10.
 DR P-PSDB; AAY56856.

PT A protein having antigenicity of canine distemper virus nucleocapsid
 XX protein - useful in the diagnosis of canine distemper virus infection.

PS Disclosure; Page 10-11; 15pp; Japanese.

XX The invention provides a protein which has a molecular weight of 58 kD
 CC and has antigenicity of nucleocapsid protein (NP) of canine distemper
 CC virus (CDV) belonging to Morbillivirus genus of Paramyxovirus family. The
 CC protein can be used to prepare a reagent for the determination of anti-
 CC CDV NP antibody by immobilizing the above protein on a carrier or a
 CC membrane as the active component. The reagent can be used for diagnosis
 CC of CDV infection, judgement of effect of vaccine and judgement of
 CC inoculation period. The reagent can determine anti-CDV NP antibody
 CC contained in canine serum easily. The present sequence represents a
 CC nucleotide sequence encoding the Morbillivirus antigenic protein.
 CC (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 1736 BP; 523 A; 386 C; 401 G; 426 T; 0 U; 0 Other;

Query Match 7.4%; Score 109.2; DB 3; Length 1736;
 Best Local Similarity 47.5%; Pred. No. 4.6e-23;
 Matches 324; Conservative 0; Mismatches 359; Indels 0; Gaps 0;

QY 499 TCTATCCAGGCTCAGGTATGGTGCACAGTACGAGGCGCAATACGCGAGGTGGAGCTCC 558
 DB 510 TCCATCTGGCTCAAAATTGGATCTGCTAGCTAAGCGGTGATGCTCTCTGATCTGCA 569
 QY 559 GATGAGTCGGAACAAGAAGATCAATAGTACATGACGAGGCAAGCTCAGAAGAAG 618
 DB 570 GCGACTCGGAGATGAGAAGGTGATTAGTATATACCCAGCAAGACGTGTGTCGGAGAA 629
 QY 619 TACATCTCCACCTGTATGACGAGTGCATTCACACTCAATCAACATCAATCTCTGCGCA 678
 DB 630 TTTAGAATGAACAAATCTGGCTTGATTTAGTAAACAGGATTGCTGAGGACCTATCT 689
 QY 679 GTCCGCAATTTCTTAGTACGAGCTTAAGAGAGCGCGCAATACGCGAGGTGGAGCTCC 738
 DB 690 TTGAGGCGATTCATGTGGCACTCATTTTGACATCAAAAGATCCCGAGGAACACCT 749
 QY 739 ACGTATTACACTTAGTAGGGATGTAGACTCATATCAGGAAACACCGACTTACTGCA 798
 DB 750 AGAATTGCTGAATGATTTGTGTATATAGATAAATCACTTGTGAAGCTGGTGTAGCTAGT 809
 QY 799 TTCTTCTTACACTCAAAATATGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGC 858
 DB 810 TTCACTCAACTATCAAGTTTGGCATGAACATATGATTCGGCTCTTTGGGTGGCATGAG 869
 QY 859 CTCACAGGCGATATCAAAAGATGAAGCAGCTCATGCTTTATATCGGATGAAGGGAGAA 918
 DB 870 TTTTCGGGAATTAACAACATATTGAATCCCTCATGATGCTATATCAACAGATGGGTGAA 929
 QY 919 AATGCGCGGTACATGACATTTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 978
 DB 930 ACGACCATACATGTTTATCTTTGGAAACCTCTGTTCAAAACAAATTTAGTCAGGCTCC 989
 QY 979 TATGCAACAGCTTTATCTTTTGGCATGGGCGATCGCATCTCTTATAGTAAGAACTGGC 1038
 DB 990 TACCCATTCTCGGAGTTATGCTATGGGGGTTGGTGTGAATTTAGAACTCCATGGGA 1049

QY 1039 AAATACCAATTCGCCAGAGACTTCTATGAGCAATCATCTTGAGACTCGGGGTGGAGTAT 1098
 DB 1050 GGAATTAATTTTCGTGCTGATCTTACTTTGACCCAGCCTACTTCAGACTCGGGCAAGAAATG 1109
 QY 1099 GCTCAGGCTCAGGGGAGTAGCATCAACGAGACATGGCTGCTGAGCTAAACTAACCCCG 1158
 DB 1110 GTTAGACGATCTGACAGGCAAGTAAGCTCCGCACTTGCTGCCGAGCTTGGCATCACAAG 1169
 QY 1159 GCAGCAAGAAGGGGCTCTGGCAG 1180
 DB 1170 GAGGAAGCTCAGCTGTGTCTCAG 1191

RESULT 12

ABI98955

ID ABI98955 standard; DNA; 1572 BP.

XX AC ABI98955;

XX 18-FEB-2002 (first entry)

XX Canine distemper virus, CDV, N gene.

XX Virucide; vaccine; virus; virulence; canine distemper virus; CDV;
 XX measles; dog; ds.

XX Canine distemper virus.

XX US6309647-B1.

XX 30-OCT-2001.

XX 15-JUL-1999; 99US-00354138.

XX 15-JUL-1999; 99US-00354138.

XX (AVET) AVENTIS PASTEUR.

XX Paoletti E, Tartaglia J, Taylor J, Gettig R;
 XX WPI; 2002-040232/05.

XX Novel virus, useful for inducing immune response in dog against CDV,
 XX comprises the modified recombinant virus having attenuated virulence
 XX comprising exogenous DNA sequences encoding antigens of canine distemper
 XX virus (CDV) or measles virus.

XX Claim 1; Fig 18; 147pp; English.

XX The present invention relates to modified recombinant viruses, comprising
 XX inactivated virus-encoded genetic functions so that the viruses have
 XX attenuated virulence, yet retained efficiency. The viruses can contain
 XX DNA encoding a canine distemper virus (CDV) antigen or measles M or N
 XX antigen. The recombinant viruses are useful for inducing an antigenic or
 XX immunological response in a dog or other carnivore against CDV. The
 XX present sequence was used in an example from the present invention

XX Sequence 1572 BP; 472 A; 330 C; 372 G; 398 T; 0 U; 0 Other;

Query Match 7.3%; Score 106.6; DB 6; Length 1572;
 Best Local Similarity 46.0%; Pred. No. 2.9e-22;
 Matches 361; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

QY 499 TCTATCCAGGCTCAGGTATGGTGCACAGTACGAGGCGCAATACGCGAGGTGGAGCTCC 558
 DB 505 TCCATCTGGCTCAAAATTGGATCTGCTAGCTAAGCGGTGATGCTCTCTGATCTGCA 564
 QY 559 GATGAGTCGGAACAAGAAGATCAATAGTACATGCAAGGCGAGTCCAGAAGAAG 618
 DB 565 GCGACTCGGAGATGAGAAGGTGATTAAAGTATACCCAGCAAGACGTGTGGTCGGAGAA 624
 QY 619 TACATCTCCACCTGTATGAGGAGTGCATTTCACTCACAATCAGACATTTCTTGGCA 678

Db 625 TTATGAATGACAAATCTGGCTGATATGTTTGAAGACAGGATGCTGAGACCTATCT 684
Qy 679 GTCCGCAATTTCTTAGTTAGCGAGCTTAAAGAGAGCGCGCAATACGGCAGGTGGAGCTCC 738
Db 685 TTGAGGCGAATTCATGTTGGCGCTCATCTTGACATCAACGATCCCGCAGGAACAAGCCT 744
Qy 739 ACGTATTACAACTTAGTAGGGATGATAGATCATACATCAGGAACACCGGACTTACTGCA 798
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Qy 919 AATGCGCGTACATGACATTTGCTAGGTGACAGTGCATCAGATGAGCTTTGCACCGCTGAG 978
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Qy 1099 GCTCAGGCTCAGGGAGTAGCATCAACGAAGACATGCTGCTGAGCTTAAACTAACCCCG 1158
Db 1105 GTTAGGAGATCTGCGGCAAGTAGTCTGCACTTGCCTGCGGAGCTTGGCATCACCAG 1164
Qy 1159 GCAGCAAGAGGGCGCTGGCAGCTGCTGCCCAACGAGTGTCTGAGGAACCTGGCAGCGTG 1218
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Qy 1279 TCTCA 1283
Db 1285 AATCA 1289

RESULT 13

ABK15038
ID ABK15038 standard; cDNA; 15690 BP.

XX AC
XX AC
XX AC
XX AC

DT 08-MAY-2002 (first entry)

XX Canine distemper virus cDNA.

DE CDV; ss; antiviral; immunostimulant; immunogen; vaccine; gene therapy;
XX progressive demyelinating disease; Paget's disease; multiple sclerosis.

XX Canine distemper virus.

XX WO200200883-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US020157.

XX 23-JUN-2000; 2000US-0213698P.

XX (AMCY) AMERICAN CYANAMID CO.

XX

PI Parks CL, Sidhu MS, Walpita P, Kovacs GR, Udem SA;
XX WPI; 2002-130895/17.

XX Producing recombinant canine distemper virus (CDV), useful in gene
PT therapy, comprises transfecting cell with transcription vector containing
PT nucleic acid encoding CDV genome or antigenome.

XX Claim 43; Fig 6; 109pp; English.

CC The invention relates to producing a recombinant canine distemper virus
CC (CDV) comprising transcribing/transfecting a cell with a composition
CC containing: (a) a transcription vector containing an isolated nucleic
CC acid molecule encoding a genome/antigenome of CDV, or its variant
CC sequence; and (b) an expression vector with an isolated nucleic acid
CC molecule encoding the trans-acting proteins (N, P and L) for
CC encapsidation, transcription and replication. The recombinant CDV is used
CC as an immunogen for immunising an animal or human against CDV. Also
CC included are a plasmid comprising a CDV genome/antigenome or encoding CDV
CC proteins, and a host cell transformed with the vector. The recombinant
CC virus are useful as vectors for expressing foreign genetic information,
CC e.g. foreign genes, for applications including immunogenic or
CC pharmaceutical compositions for pathogens other than canine distemper,
CC gene therapy, and cell targeting. The recombinant CDVs are also used in
CC generating antibodies, prophylactic and therapeutic applications,
CC specifically in treating or ameliorating canine distemper infection
CC (which causes a progressive demyelinating disease with neurological
CC symptoms and is implicated in human multiple sclerosis and Paget's
CC disease), and in preparing mutant virus and immunogenic compositions.
CC Protein and nucleotide sequences may be used to design screening systems
CC for compounds that interfere or disrupt normal virus development, via
CC encapsidation, replication, or amplification. The present sequence is the
CC Canine distemper virus entire cDNA sequence

XX SQ Sequence 15690 BP; 4810 A; 3355 C; 3387 G; 4138 T; 0 U; 0 Other;

Query Match 7.3%; Score 106.6; DB 6; Length 15690;
Best Local Similarity 46.0%; Pred. No. 1.1e-21;
Matches 361; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

Qy 499 TCTATCCAGGCTCAGGTATGGTCCAGTAGCGAAGCGCATGACTGCATATGACAGCA 558
Db 612 TCCATCTGGCTCAATTTGGATCCTGCTAGTAAGCGGTGACTGCTCTCTGATATGCA 671
Qy 559 GATGAGTCGGAACAAGAGAAATCAATAGTACATGCGAGGAGGAGAGTCCAGAGAG 618
Db 672 GCCGACTCGGAGATGAGAAAGGTGGAATTAAGTATACCCAGCAAGACGCTGGTGGAGAA 731
Qy 619 TACATCTCCACCTGTATGCGAGGTGCAATTCAACTCAACAATCAGACATTTCTTGCA 678
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QY 1159 GCAGCAAGAGGGGCTCGGAGCTGCTGCCAACAGAGTGTCTGAGAAACTGGCAGCGTG 1218
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QY 1219 GATATTCTTACTCAACAGCGGGTCTCTCACTGGGCTCAGCATGGAGGCCCGGAGCC 1278
Db 1332 GCTACTGGTCTTAAGCAATCCCAATCACTTTTCTGCACTCGGAAAGATCCGAAATCGCC 1391
QY 1279 TCTCA 1283
Db 1392 AATCA 1396

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RESULT 14

ABK15000
ID ABK15000 standard; DNA; 15690 BP.

AC ABK15000;

XX 08-MAY-2002 (first entry)

DE Canine distemper virus positive, antigenomic strand.

XX CDV; ss; antiviral; immunostimulant; antigenomic strand; immunogen;

KW vaccine; gene therapy; progressive demyelinating disease;

KW Page's disease; multiple sclerosis.

XX Canine distemper virus.

XX WO200200883-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US020157.

XX 23-JUN-2000; 2000US-0213698P.

XX (AMCY) AMERICAN CYANAMID CO.

XX Parks CL, Sidhu MS, Walpita P, Kovacs GR, Udem SA;

XX WPI; 2002-130895/17.

PT Producing recombinant canine distemper virus (CDV), useful in gene
therapy, comprises transfecting cell with transcription vector containing
nucleic acid encoding CDV genome or antigenome.

PS Claim 21; Page; 109pp; English.

XX The invention relates to producing a recombinant canine distemper virus
(CDV) comprising transforming/transfecting a cell with a composition
containing: (a) a transcription vector containing an isolated nucleic
acid molecule encoding a genome/antigenome of CDV, or its variant
sequence; and (b) an expression vector with an isolated nucleic acid
molecule encoding the trans-acting proteins (N, P and L) for
encapsulation, transcription and replication. The recombinant CDV is used
as an immunogen for immunising an animal or human against CDV. Also
included are a plasmid comprising a CDV genome/antigenome or encoding CDV
proteins, and a host cell transformed with the vector. The recombinant
virus are useful as vectors for expressing foreign genetic information,
e.g. foreign genes, for applications including immunogenic or
pharmaceutical compositions for pathogens other than canine distemper,

CC gene therapy, and cell targeting. The recombinant CDVs are also used in
CC generating antibodies, prophylactic and therapeutic applications,
CC specifically in treating or ameliorating canine distemper infection
CC (which causes a progressive demyelinating disease with neurological
CC symptoms and is implicated in human multiple sclerosis and Paget's
CC disease), and in preparing mutant virus and immunogenic compositions.
CC Protein and nucleotide sequences may be used to design screening systems
CC for compounds that interfere or disrupt normal virus development, via
CC encapsidation, replication, or amplification. The present sequence is the
CC canine distemper virus positive, antigenomic strand. Note: The present
CC sequence is not shown in the specification but was obtained from Genbank
CC using accession number AF014953
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SQ Sequence 15690 BP; 4809 A; 3355 C; 3388 G; 4138 T; 0 U; 0 Other;

Query Match 7.3%; Score 106.6; DB 6; Length 15690;
Best Local Similarity 46.0%; Pred. No. 1.1e-21;
Matches 361; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

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QY 499 TCTATCCAGGCTCAGTATGGGTACAGTAGCGAAGGCCATGACTGCATATGAGCAGCA 558
Db 612 TCACTCTGGCTCAAAATTTGGATCTCTAGTAAAGCGGTGACTCTCTGATCTGCA 671
QY 559 GATGAGTCGGAACAAGAGAAATCAATAGTACATGTCAGCAAGCGCAGAGTCCAGAGAAG 618
Db 672 GCCGACTCGGAGATGAGAAGGTGGATTAGTATATCCAGCAAAAGAGCTGTGGTCGAGAA 731
QY 619 TACATCCTCCACCCTGTATGAGGAGTGCATTAATCACTCAATCAGACATCTCTCTGGCA 678
Db 732 TTTAGAAATGAACAAAATCTGGCTTGATATTTAGAAACAGGATTTGCTGAGGACCTATCT 791
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QY 739 AGTATTACAACTTAGTAGGGGATGTAGACTCATATCAGGAACACCGGACTTACTTGCA 798
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QY 859 CTCACAGCGATATCCAAAAGATGAAGCAGCTCATGCGTTTATATATCGGATGAAGAGAA 918
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Db 1332 GCTACTGGTCTTAGCAATCCCAATCACTTTCTGCACTCGGAAAGATCCGAAATCGCC 1391
QY 1279 TCTCA 1283

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Db 1392 AATCA 1396

RESULT 15

ABK15039

ID ABK15039 standard; DNA; 18826 BP.

XX ABK15039;

XX 08-MAY-2002 (first entry)

XX Canine distemper virus full length genomic clone plus vector.

XX CDV; ds; antiviral; immunostimulant; immunogen; vaccine; gene therapy;
 KW progressive demyelinating disease; Paget's disease; multiple sclerosis.

XX Canine distemper virus.

PH Key Location/Qualifiers

FT misc_feature 1..2198

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FT /note= "Vector sequence"

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FT /*tag= b

FT /note= "Vector sequence"

XX WO200200883-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US020157.

XX 23-JUN-2000; 2000US-0213698P.

XX (AMCY) AMERICAN CVANAMID CO.

XX Parks CL, Sidhu MS, Walpita P, Kovacs GR, Udem SA;

XX WPI; 2002-130895/17.

XX Producing recombinant canine distemper virus (CDV), useful in gene
 PT therapy, comprises transfecting cell with transcription vector containing
 PT nucleic acid encoding CDV genome or antigenome.

XX Claim 43; Fig 7; 109pp; English.

XX The invention relates to producing a recombinant canine distemper virus
 CC (CDV) comprising transforming/transfecting a cell with a composition
 CC containing: (a) a transcription vector containing an isolated nucleic
 CC acid molecule encoding a genome/antigenome of CDV, or its variant
 CC sequence; and (b) an expression vector with an isolated nucleic acid
 CC molecule encoding the trans-acting proteins (N, P and L) for
 CC encapsidation, transcription and replication. The recombinant CDV is used
 CC as an immunogen for immunising an animal or human against CDV. Also
 CC included are a plasmid comprising a CDV genome/antigenome or encoding CDV
 CC proteins, and a host cell transformed with the vector. The recombinant
 CC virus are useful as vectors for expressing foreign genetic information,
 CC e.g. foreign genes, for applications including immunogenic or
 CC pharmaceutical compositions for pathogens other than canine distemper,
 CC gene therapy, and cell targeting. The recombinant CDVs are also used in
 CC generating antibodies, prophylactic and therapeutic applications,
 CC specifically in treating or ameliorating canine distemper infection
 CC (which causes a progressive demyelinating disease with neurological
 CC symptoms and is implicated in human multiple sclerosis and Paget's
 CC disease), and in preparing mutant virus and immunogenic compositions.
 CC protein and nucleotide sequences may be used to design screening systems
 CC for compounds that interfere or disrupt normal virus development, via
 CC encapsidation, replication, or amplification. The present sequence is the
 CC Canine distemper virus entire genomic DNA sequence plus vector sequences

SQ Sequence 18826 BP; 5565 A; 4157 C; 4188 G; 4916 T; 0 U; 0 Other;

Query Match

7.3%; Score 106.6; DB 6; Length 18826;

Best Local Similarity 46.0%; Pred. No. 1.2e-21;
 Matches 361; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

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Qy	919	AATGCGCGTACATGACATTTGCT	AGAGTACAGATGAGCTTTGCACCGGCTGAG	978
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Qy	1039	AAATACCAATTCGCCAGAGACT	TTATGAGCAATCATTTCTGGAGACTCGGGGTGGAGTAT	1098
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Qy	1159	GCAGCAAGAGGGGCTTGGCAG	CTGCTGCCCAACGAGTGTCTGAGGAAACTGGCGAGCTG	1218
Db	3470	GAGGAAGCTCAGCTAGTGT	TCAGAAATAGCATCCAAAGACACAGAGGACCGACAAATTCGA	3529
Qy	1219	GATATTCCTACTCAACAGCG	GGGGTCTCTCACTGGGTTCAGCGATGAGGCCCCCGAGCC	1278
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Qy	1279	TCCTCA 1283		
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GenCore version 5.1.6
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

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gene, complete cds.
AF284646.1 GI:12382261
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
1 (bases 1 to 1470)
Kho,C.I., Tan,W.S. and Yusoff,K.
Direct Submission

JOURNAL

Submitted (03-JUL-2000) Biochemistry and Microbiology, University
Putra Malaysia, Faculty of Science and Environmental Studies,
Serdang, Selangor 43400, Malaysia

FEATURES

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ORIGIN

Query Match 100.0%; Score 1470; DB 14; Length 1470;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 2

AF419402

LOCUS

DEFINITION

Newcastle disease virus chicken/Italy/Milano/45 nucleocapsid

protein gene, complete cds.

AF419402

ACCESSION

AF419402.1

VERSION

AF419402.1

KEYWORDS

ORGANISM

REFERENCE

1746 bp RNA linear VRL 21-PEB-2002

Newcastle disease virus chicken/Italy/Milano/45 nucleocapsid

protein gene, complete cds.

AF419402

AF419402.1

GI:15811671

Newcastle disease virus

Newcastle disease virus

Viruses; ssRNA negative-strand viruses; Mononegavirales;

Paramyxoviridae; Paramyxovirinae; Rubulavirus.

1 (bases 1 to 1746)

Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Nucleotide sequence analysis of the Newcastle disease virus
nucleocapsid protein gene and phylogenetic relationships among the
Paramyxoviridae
Virus Res. 83 (1-2), 119-129 (2002)
21854562
11864745
2 (bases 1 to 1746)
Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Direct Submission
Submitted (14-SEP-2001) Agricultural Research Service, USDA,
Southeast Poultry Research Laboratory, 934 College Station Road,
Athens, GA 30605, USA

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ORIGIN

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QY	61	GCTCACGGAGGGGAGAGACAGGAGCACTTTAAGAGTTGAGGTCAGGTCCTCAGTATTCACCTTT	120	
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QY	121	AACAGTGCAGATCCAGAGATAGATGAAATTTTCGGGTATTTCTGTCTTCGGATGTCGTT	180	
Db	187	AACAGTGTATATCCAGAAGACAGATGGAATTTTCGGGTATTTCTGTCTTCGGATGTCGTT	246	
QY	181	AGCGAGAGCCCAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTCTGTGCTCCCAT	240	
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QY	241	TCTCAAGTGATGAGGAACCATGTTGCCCTTCAGGAGAAAACAGATGAGGCTACACTACT	300	
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QY	301	GTCTCTTGAGATCGATGGTTTTACACAGACGGTGCCTCAGTTTCAACACAGAGTGGGGTG	360	
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QY	421	AACGGTACTCCGTTTCGTACGGCTGGGGTTGAGATGATGCACACAGAGATATCACTGAT	480	
Db	487	AATGGTACTCCGTTTCGTACAGCTGGGGTTGAGATGATGCACACAGAGATATCCCGAT	546	
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[illegible]

RESULT 3
AF419404
LOCUS
DEFINITION
ACCESSION

VERSION	AF419404.1	GI:15811675	
KEYWORDS	Newcastle disease virus		
SOURCE	Newcastle disease virus		
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.		
REFERENCE	1 (bases 1 to 1700)		
AUTHORS	Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.		
TITLE	Nucleotide sequence analysis of the Newcastle disease virus nucleocapsid protein gene and phylogenetic relationships among the Paramyxoviridae		
JOURNAL	Virus Res. 83 (1-2), 119-129 (2002)		
MEDLINE	21854562		
PUBMED	11864745		
REFERENCE	2 (bases 1 to 1700)		
AUTHORS	Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-SEP-2001) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA		
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Best Local Similarity	92.2%;	Pred. No. 0;	
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QY	61	GCTCAGCGAGGGGAGAGAGGAGGAGCACTTTAAGAGTTGAGTCCCAAGTATCACTCTT	120
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QY	121	AACAGTGACGATCCAGAGATAGATGGAAATTTTCGGTATTCTGTCTTCGAGTTCTGTT	180
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DB	367	ATTCTTGAGATTGATGGTTTACCAACAGCAGCGCCCAAGTTCAACAACAGGAGTGGAGT	426
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DB	427	TCCGAGGAGAGGACAGAGATTCAATGCTGTAGCAGGATCTCCCTCGGCGGTGAGT	486
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RESULT 4
LOCUS AF419405
DEFINITION Newcastle disease virus chicken/Mexico/37821/96 nucleocapsid
protein gene, complete cds.
ACCESSION AF419405
VERSION AF419405.1 GI:15811677
SOURCE Newcastle disease virus
ORGANISM Newcastle disease virus
VIRUSES; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
REFERENCE 1 (bases 1 to 1746)
AUTHORS Seal,B.S., Crawford,J.M., Sellers,H.S., Locke,D.P. and King,D.J.
TITLE Nucleotide sequence analysis of the Newcastle disease virus
nucleocapsid protein gene and phylogenetic relationships among the
Paramyxoviridae
JOURNAL Virus Res. 83 (1-2), 119-129 (2002)
MEDLINE 21854562
PUBMED 11864745
REFERENCE 2 (bases 1 to 1746)
AUTHORS Seal,B.S., Crawford,J.M., Sellers,H.S., Locke,D.P. and King,D.J.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2001) Agricultural Research Service, USDA,
Southeast Poultry Research Laboratory, 934 College Station Road,
Athens, GA 30605, USA
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 AJ306303
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 KEYWORDS NP gene; nucleoprotein.
 SOURCE Newcastle disease virus
 ORGANISM Newcastle disease virus
 Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 REFERENCE 1
 AUTHORS Barbezange, C. and Jestin, V.
 TITLE Molecular characterisation of three avian paramyxovirus type 1 isolated from pigeons in France
 JOURNAL Virus Genes 26 (2), 175-183 (2003)
 MEDLINE 22687690
 PUBMED 12803469
 REFERENCE 2 (bases 1 to 1580)
 AUTHORS Barbezange, C.
 TITLE Direct Submission
 JOURNAL Submitted (07-FEB-2001) Barbezange C., VIPAC, AFSSA Site de Ploufragan, BP53, 22440 Ploufragan cedex, FRANCE
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gene

CDS

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RESULT 7
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LOCUS
DEFINITION
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protein gene, complete cds.
ACCESSION
AF419406
VERSION
AF419406.1 GI:15811679
KEYWORDS
Newcastle disease virus
SOURCE
Newcastle disease virus
ORGANISM
Viruses; SRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
1 (bases 1 to 1557)
Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Nucleotide sequence analysis of the Newcastle disease virus
nucleocapsid protein gene and phylogenetic relationships among the
Paramyxoviridae
Virus Res. 83 (1-2), 119-129 (2002)
21854562
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2 (bases 1 to 1557)
Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Direct Submission
Submitted (14-SEP-2001) Agricultural Research Service, USDA,
Southeast Poultry Research Laboratory, 934 College Station Road,
Athens, GA 30605, USA
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FEATURES
source

CDS

ORIGIN

Query Match 86.3%; Score 1268.4; DB 14; Length 1557;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
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VERSION AJ306302.1 GI:28268508
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ORGANISM Newcastle disease virus
VIRUSES; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
REFERENCE 1
Barbezange, C. and Jestin, V.
Molecular characterisation of three avian paramyxovirus type 1
isolated from pigeons in France
Virus Genes 26 (2), 175-183 (2003)
MEDLINE 22687690
PUBMED 12803469
REFERENCE 2 (bases 1 to 1580)
Barbezange, C.
Direct Submission
AUTHORS Submitted (07-FEB-2001) Barbezange C., VIPAC, AFSSA Site de
Ploufragan, BP53, 22440 Ploufragan cedex, FRANCE
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Best Local Similarity 91.3%; Pred. No. 0;
Matches 1342; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
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DEFINITION	protein gene, complete cds.		
ACCESSION	AF419407		
VERSION	AF419407.1	GI:15811681	
KEYWORDS	Newcastle disease virus		
SOURCE	Newcastle disease virus		
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Rubulavirus.		
REFERENCE	1 (bases 1 to 1488)		
AUTHORS	Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.		
TITLE	Nucleotide sequence analysis of the Newcastle disease virus nucleocapsid protein gene and phylogenetic relationships among the Paramyxoviridae		
JOURNAL	Virus Res. 83 (1-2), 119-129 (2002)		
MEDLINE	21854562		
PUBMED	11864745		
REFERENCE	2 (bases 1 to 1488)		
AUTHORS	Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-SEP-2001) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA		
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RESULT 10
LOCUS AF419396 1585 bp RNA linear VRL 21-FEB-2002
DEFINITION Newcastle disease virus parrot/U.S. (IL)/27994/91 nucleocapsid
protein gene, complete cds.
ACCESSION AF419396
VERSION AF419396.1 GI:15811659
KEYWORDS
SOURCE
ORGANISM Newcastle disease virus
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
REFERENCE
1 (bases 1 to 1585)
AUTHORS Seal,B.S., Crawford,J.M., Sellers,H.S., Locke,D.P. and King,D.J.
TITLE Nucleotide sequence analysis of the Newcastle disease virus
nucleocapsid protein gene and phylogenetic relationships among the
Paramyxoviridae
JOURNAL Virus Res. 83 (1-2), 119-129 (2002)
MEDLINE 21854562
PUBMED 11864745
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REFERENCE

2 (bases 1 to 1585)
Seal,B.S., Crawford,J.M., Sellers,H.S., Locke,D.P. and King,D.J.
Direct Submission
Submitted (14-SEP-2001) Agricultural Research Service, USDA,
Southeast Poultry Research Laboratory, 934 College Station Road,
Athens, GA 30605, USA

FEATURES

Location/Qualifiers

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Query Match 85.5%; Score 1257.2; DB 14; Length 1585;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 1337; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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gene, complete cds.
ACCESSION AF419401
VERSION AF419401.1 GI:15811669
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SOURCE Newcastle disease virus
ORGANISM Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
REFERENCE 1 (bases 1 to 1694)

AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Nucleotide sequence analysis of the Newcastle disease virus
nucleocapsid protein gene and phylogenetic relationships among the
Paramyxoviridae
Virus Res. 83 (1-2), 119-129 (2002)
21854562
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2 (bases 1 to 1694)
Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Direct Submission
Submitted (14-SEP-2001) Agricultural Research Service, USDA,
Southeast Poultry Research Laboratory, 934 College Station Road,
Athens, GA 30605, USA
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VERSION
KEYWORDS
SOURCE
ORGANISM

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Newcastle Disease virus strain ZJ1, complete genome.
AF431744
AF431744.3 GI:28933797

Newcastle disease virus
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.

REFERENCE

1 (bases 1 to 15192)
Huang, Y., Wu, Y., Wan, H. and Liu, X.
Complete nucleotide sequence of a NDV strain of goose origin (ZJ1)
Unpublished

AUTHORS

2 (bases 1 to 15192)
Huang, Y., Wu, Y., Wan, H. and Liu, X.
Direct Submission

JOURNAL

Submitted (10-OCT-2001) Animal Infectious Disease Laboratory,
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AUTHORS

3 (bases 1 to 15192)
Huang, Y., Wu, Y., Wan, H. and Liu, X.
Direct Submission

JOURNAL

Submitted (10-MAR-2003) Animal Infectious Disease Laboratory,
Yangzhou University, 12 Wenhui East Road, Yangzhou, Jiangsu 225009,
P.R. China

REMARK

Sequence update by submitter

REFERENCE

4 (bases 1 to 15192)
Huang, Y., Wu, Y., Wan, H. and Liu, X.
Direct Submission

AUTHORS

Submitted (13-MAR-2003) Animal Infectious Disease Laboratory,
Yangzhou University, 12 Wenhui East Road, Yangzhou, Jiangsu 225009,
P.R. China

JOURNAL

Nucleotide and amino acid sequences updated by submitter
On Mar 13, 2003 this sequence version replaced gi:28911872.

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AF419400
LOCUS
DEFINITION
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ACCESSION
AF419400
VERSION
AF419400.1 GI:15811667
KEYWORDS
Newcastle disease virus

ORGANISM Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
REFERENCE
1 (bases 1 to 1694)
Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Nucleotide sequence analysis of the Newcastle disease virus nucleocapsid protein gene and phylogenetic relationships among the Paramyxoviridae
Virus Res. 83 (1-2), 119-129 (2002)
MEDLINE
21854562
PUBMED
11864745
REFERENCE
2 (bases 1 to 1694)
Seal, B.S., Crawford, J.M., Sellers, H.S., Locke, D.P. and King, D.J.
Direct Submission
Submitted (14-SEP-2001) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
7328.827 Million cell updates/sec

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Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1154.8	78.6	15900	13	US-10-440-419-55
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ALIGNMENTS

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; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, SIBA K.
; APPLICANT: HUANG, ZHUHUI
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; TITLE OF INVENTION: VACCINES OR VACCINE VECTORS
; FILE REFERENCE: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 15882
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-56

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; Sequence 3, Application US/10415981
; Publication No. US20040043035A1
; GENERAL INFORMATION:
; APPLICANT: AKZO No. US20040043035A1el N.V.
; TITLE OF INVENTION: A recombinant Newcastle disease virus nucleoprotein
; TITLE OF INVENTION: mutant as a marker vaccine
; FILE REFERENCE: 2000583
; CURRENT APPLICATION NUMBER: US/10/415,981
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (122)...(1588)
; OTHER INFORMATION: NP gene: nucleotides 56-1801; NP coding sequence:
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US-10-415-981-3

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Db 1856 CTAGATAAAGGTACTCGGAAATACCAATTTGCGAGGACTTTATGAGCACATCATCTCGG 1915
QY 1081 AGACTCGGGTGGAGTATGCTCAGGCTCAGGGGAGTAGCATCAACGAAGACATGGCTGCT 1140
Db 1916 AGACTTTGGAGTAGAGTACGCTCAGGCTCAGGGAAAGTAGCATTAACCGAGGATATGGCTGCC 1975
QY 1141 GAGCTAAAGTAAACCCCGGACGAAGAGGGGCTCGGAGCTGCTGCCCAACGAGGTGCT 1200
Db 1976 GAGCTAAAGCTAAACCCCGAGCAGAGAGGGGCTCGGAGCTGCTGCCCAACGAGGTCTCC 2035
QY 1201 GAGGAACTGGCAGCGTGGATATTCCTACTCAACAGCCGGGTCTCTCACTGGGCTCAGC 1260
Db 2036 GAGGAGCCAGCAGCATAGACATGCTCTCAACAGTCCGAGTCTCACTGGGCTTAGC 2095
QY 1261 GATGAGGCCCCGAGCCTCTCAGGTTGATCGAACAAGTCGCAAGGGGCAACAGATGCC 1320
Db 2096 GAGGGGGGGTCCCAAGCTCTCAAGGGCGATCGAATAGATCGCAAGGGGCAACAGAGGCC 2155
QY 1321 GGAGATGGGGAGACCAATTTCTTGGATTTGATGAGAGCAGTGGCGAACAGCATGCGAGAA 1380
Db 2156 GGGGATGGGGAGACCCCAATTTCTTGGATTTGATGAGAGGCTAGCAATAGCATGAGGGAG 2215
QY 1381 GCGCCAACTCCGACAGACACCAACCCCGGAAACCCCGGACTCCCGGGCCATCA 1440
Db 2216 GCGCCAACTCTGACAGGCACTCCCAATTCGGGCTCCCGCAACTCTCGGGCCATCC 2275
QY 1441 CAAGATACGACACCGGCTGGGGTATGA 1470
Db 2276 CAAGATACGACACCGGCTGGGGTATTTGA 2305
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```
RESULT 4
US-09-741-744A-134
; Sequence 134, Application US/09741744A
; Publication No. US20030087417A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus
; APPLICANT: de Leeuw, Olav
; APPLICANT: Klaus, Guus
; APPLICANT: Arnaud, Gielkens
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnost
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/09/741,744A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus LaSota
US-09-741-744A-134
```

```
Query Match 78.1%; Score 1148.4; DB 10; Length 15186;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
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QY 1 ATGCTTCCGTTATTCGATGATATACGAGCAGCTCTCGCTGCTCAGACTCGCCCCCATGGA 60
Db 122 ATGCTTCCGTTATTCGATGATATACGAGCAGCTCTCGGGCTCAGACTCGCCCCCATGGA 181
QY 61 GCTCAGGAGGGGAGAGAGGAGGAGCACTTTAAAGATTGAGTCCAGTCCAGTATTCACCTCT 120
Db 182 GCTCATGAGGGGGAGAAAAGGAGATCTTTAAAGTAGAGAGTCCCTGAGGATTCACCTCT 241
QY 121 AACAGTGAAGTCCAGAGATAGATGGAATTTTTCGGTATTCGTCTTCGGATTCGTCT 180
Db 242 AACAGTGAAGTCCAGAGATAGATGGAATTTTTCGGTATTCGTCTTCGGATTCGTCT 301
QY 181 ACGGAGGAGCCCAACAAACCGCTCAGGCAAGGTGCTCTCATATCCCTCTGCTGCCCAT 240
Db 302 ACGGAGATGCCCAACAAACCACTCAGGCAAGGTGCTCTCATATCTCTTTTGTCTCCAC 361
QY 241 TCTCAAGTATCAGGAACCATGTTGCCCTTCAGGAAACAGAAATGAGGCTACACTGACT 300
Db 362 TCACAGGTAATGAGGAACCATGTTGCCATTGAGGAAACAGAAATGAGGCTACACTGACT 421
QY 301 GTTCTTGAGATCGATGTTTACACGAGCGTCCCTCAGTTCACAAACAGGAGTGGGTG 360
Db 422 GTGCTTGAGATTGATGCTTTGCCAACGCGCCAGTTCACAAATAGGAGTGGAGTG 481
QY 361 TCTGAGGAGAGACACAGAGATTCATGTTGATAGAGGGTCTCTCCCTCGGGCTCAGT 420
Db 482 TCTGAGAGAGAGACACAGAGATTTGCGATGATAGAGGATCTCTCCCTCGGGATCAGC 541
QY 421 AACGGTACTCCGTTCTGCTCAGCGGTGGGTTTGAAGATGATGACCAAGAGATATCACTGAT 480
Db 542 AACGGAACCCCGTTCTGCTACACCGGGGAGAGATGATGACCAAGAGATCAACGAT 601
QY 481 ACTCTGGAAGAAATCCTGCTATTCAGGCTCAGGTATGGGTACAGTAGGAAGGCCATG 540
Db 602 ACCCTGGAGAGTCTCTCTATCCAGGCTCAGTATGGGTACAGTAGCAAAAGCCATG 661
QY 541 ACTGCATATGACACAGCAGATGATCGGAAACAAAGAAAGATCAATTAAGTACATGCGACAA 600
Db 662 ACTGCGTATGAGACTCGAGATGATCGGAAACAAAGGCGAATCAATTAAGTATATGACAA 721
QY 601 GGCAGAGTCCAGAAAGATACATCTCTCCACCTCTGATGCGAGGAGTGCATTTCACTCA 660
Db 722 GGCAGGGTCCAAAGAAATACATCTCTACCCCGTATGCGAGGAGCAAAATCACTCAG 781
QY 661 ATCAGACATCTCTCGGAGTCCGCAATTTCTTAGTTAGCGAGCTTAAGAGAGCCGCAAT 720
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Db 782 ATCAGACAGTCTCTTGGCAGTCCGCTCTTTTGGTTAGCGAGCTCAAGAGAGCGCCGAC 841
Qy 721 ACGGAGGTGGGAGCTCCAGGTATTACAACTTAGTAGGGAGTAGACTCATACATCAGG 780
Db 842 ACGGAGGTGGGAGCTCTACTTATTATTAACCTGGTAGGGAGTAGACTCATACATCAGG 901
Qy 781 AACACCGGACTTACTGCACTTCTTCTTACACTCAAAATATGGAATTAATACCAAGACATCA 840
Db 902 AATACCGGCTTACTGCACTTCTTCTGACACTCAGTACGGAATCAACCAAGACATCA 961
Qy 841 GCCCTAGCACTCAGCAGCTCTCAGCGATATCCAAAGATGAAGCAGCTCATGCGTTTA 900
Db 962 GCCCTTGCACCTTAGTAGCTCTCAGCGACATCCAGAGATGAAGCAGCTCATGCGTTG 1021
Qy 901 TATCGGATGAAGGAGAAATCGCGGTACATGACATTTCTTTGGCATGGGATGACAGTATCAGATG 960
Db 1022 TATCGGATGAAGGAGAAATCGCGGTACATGACATTTCTTTGGTATGATGACAGATG 1081
Qy 961 AGCTTTGACCGGCTGAGTATGACAGCTTTTATTTCTTTGGCATGGGATGACAGTATCAGTATC 1020
Db 1082 AGCTTTGCGCTGCGGATGATGACACATTTTCTTTGGCATGGGATGACAGTATGACAGTATC 1141
Qy 1021 TTAGATAAGGAATGGCAATATCAATTTGCGCAGAGCTTTCATGAGCAGATCATTTCTGG 1080
Db 1142 CTAGATAAGGATCTGGGAAATATCAATTTGCGCAGAGCTTTCATGAGCAGATCATTTCTGG 1201
Qy 1081 AGACTCGGGTGGAGTATGCTCAGGCTCAGGGAGTAGCATCAACGAAGACATGCGTCTGCT 1140
Db 1202 AGACTTGGAGTAGAGTATGCTCAGGCTCAGGGAGTAGCATCAACGAAGACATGCGTCTGCT 1261
Qy 1141 GAGCTAAACTAACCCCGGACAGAAAGGCGCTTGGCAGCTGCTGCGCAACGAGTGTCT 1200
Db 1262 GAGCTAAAGCTAACCCCGGACAGAAATGAAGGCGCTTGGCAGCTGCTGCGCAACGAGTGTCT 1321
Qy 1201 GAGAACTGGCAGGTGGATTTCTTACTCAACGAAGCGGGTCTCTCACTGGGCTTACG 1260
Db 1322 GACGATACAGCAGCATATATGCTTACTCAACGAAGCGGAGTCTCTCACTGGGCTTACG 1381
Qy 1261 GATGAGGCGCCGAGCTCTCAGGCTGATGCGAAGTGGGAGTCTCTCACTGGGCTTACG 1320
Db 1382 GAGGGGGTCCCAAGCTCTCAAGGGGATGCGAATAGATGCGAAGGGCAACCGAAGCC 1441
Qy 1321 GGAGATGGGAGACCCCAATTTCTGATTTGATGAGAGCAGTGGGCAACAGCATCGGAA 1380
Db 1442 GGGATGGGAGACCCCAATTTCTGATTTGATGAGAGGCTGAGCAATAGCATGAGGAG 1501
Qy 1381 GCGCCAACTCCGACAGAGCACCCACCGGAAACCCCGGAGTCTCCCGGCGCCATCA 1440
Db 1502 GCGCCAACTCTGACAGGCACTCCCAATCGGGGCTCTCCCAACTCTCTGGGCCATCC 1561
Qy 1441 CAAGATAACGACCGGACTGGGGTATTGA 1470
Db 1562 CAAGATAACGACCGGACTGGGGTATTGA 1591

RESULT 5

US-10-377-718-3
; Sequence 3, Application US/10377718
; Publication No. US20030175291A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuang
; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO
; FILE REFERENCE: 39734-186920
; CURRENT APPLICATION NUMBER: US/10/377,718
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus (NDV)
US-10-377-718-3

Query Match 78.1%; Score 1148.4; DB 15; Length 15186;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 1 ATGCTCTTCGTAATTCGATGAATACGAGCAGCTCTCGTGTCTCAGACTCGGCCCAATGGA 60
Db 122 ATGCTCTTCGTAATTCGATGAATACGAGCAGCTCTCGTGTCTCAGACTCGGCCCAATGGA 181
Qy 61 GCTCA CGGAGGGGAGAGAGAGGAGGAGCACTTTAAGAGTTGAGGTCCTCCAGTATTTCACTCTT 120
Db 182 GCTCATGAGGGGAGAGAGAGGAGGAGTACCTTTAAAGTAGAGCTCCGGTATTTCACTCTT 241
Qy 121 AACAGTACGATTCGAGAGATAGATGGAATTTTGGTATTTCTGCTTTCGGATTCGCTTT 180
Db 242 AACAGTACGATTCGAGAGATAGATGGAATTTTGGTATTTCTGCTTTCGGATTCGCTTT 301
Qy 181 AGCAGGAGCGCAACAAACCGCTCAGGCAAGTGTCTCATATCCCTCTGCTGCCAT 240
Db 302 AGCAGGAGCGCAACAAACCGCTCAGGCAAGTGTCTCATATCCCTCTGCTGCCAT 361
Qy 241 TCTCAAGTATGAGGAACCAATGTTGCCCTTGCAGGAAACAGAAATGAGGCTACACTGACT 300
Db 362 TCACAGGTAAATGAGGAACCAATGTTGCCATTCGAGGAAACAGAAATGAGGCTACACTGACT 421
Qy 301 GTTCTTGAGATCGATGTTTTCAGAGCAGCTGCTCAGTTCAACAAACAGAGTGGGTTG 360
Db 422 GTGCTTGAGATGATGTTTTCAGGCAACCGGACGCTCAGTTCAACAAATAGGAGTGGGTTG 481
Qy 361 TCTGAGGAGAGACAGAGATTCATGTTGATAGGAGTCTCTCCCTCGGCGTGCAGT 420
Db 482 TCTGAGGAGAGACAGAGATTCATGTTGATAGGAGTCTCTCCCTCGGCGTGCAGT 541
Qy 421 AACGCTACTCGTTCGTCACGCGCTGGGTTTCAAGATGATGCAACAGAAAGATATCACTCAT 480
Db 542 AACGCAACCCGTTGCTCAGAGCGGGGAGAGATGATGCAACAGAAAGATATCACTCAT 601
Qy 481 ACTCTGGAAGATTCCTGTTCTATCAGGCTCAGGTATGGGTCAAGTATGAGTATGATGAGCA 540
Db 602 ACCCTGGAGAGATTCCTCTCTATCAGGCTCAAGTATGGGTCAAGTATGAGTATGATGAGCA 661
Qy 541 ACTCATATGAGACAGAGATGATGCGGAAACAGAAAGATCAATAGTATGATGATGAGCA 600
Db 662 ACTGCTGATGAGCTGAGATGAGTGGGAAACAGAAAGATCAATAGTATGATGAGCA 721
Qy 601 GGCAAGTCCAGAAAGATGATCCTCCACCTGTATGAGGAGTGAATTTCACTTCACTACA 660
Db 722 GGCAAGTCCAGAAAGATGATCCTCCACCTGTATGAGGAGTGAATTTCACTTCACTACA 781
Qy 661 ATCAGACATTTCTGCGAGTCCGCAATTTTCTAGTACGAGCTTAAAGAGGCGGCAAT 720
Db 782 ATCAGACAGTCTCTTGGAGTCCGCAATTTTGGTATGAGGAGTCAAGAGAGGCGGCAAC 841
Qy 721 ACGGAGGTGGGAGCTCCAGTATTACAACTTAGTAGGGAGTGTAGACTCATACATCAGG 780
Db 842 ACGGAGGTGGTACCTTCTATTATTAACCTGTAGGGAGCGTAGACTCATACATCAGG 901
Qy 781 AACACCGGACTTACTGCAATTTCTTCTTACTCAATATGGAATTAATACCAAGACATCA 840
Db 902 AATACCGGCTTACTGCAATTTCTTCTTACTCAATATGGAATTAATACCAAGACATCA 961
Qy 841 GCCCTAGCACTCAGCAGCTCTCAGGCAATCAAGGATATCCAAAGATGAAGCAGCTCATGCGTTTA 900
Db 962 GCCCTTGCACCTTAGTAGCTCTCAGGCAATCAAGAGATGAAGCAGCTCATGCGTTT 1021
Qy 901 TATCGGATGAAGGAGAAATGCGGCTGATGACATGATGCTAGTGTGATGATGATGATG 960
Db 1022 TATCGGATGAAGGAGAAATGCGGCTGATGACATGATGCTAGTGTGATGATGATGATG 1081
Qy 961 AGCTTTGACCGGCTGAGTATGACAGCTTTTATTTCTTTGGCATGGGATGAGTATCAGT 1020
Db 1082 AGCTTTGCGCTGCGGATGATGACACATTTTCTTTGGCATGGGATGAGTATGAGTATCAGT 1141

Db 1442 GGGGATGGGAGACCAATTCCTGGATCTGATGAGAGCGGTAGCAAAATAGCATGAGGGAG 1501
Qy 1381 GGGCAAACTCCGACAGACACCAACCGGAAACCCCGGAGCTCCCGGGCCATCA 1440
Db 1502 GGGCAAACTCTGCACAGGCACTCCCAATCGGGGCTTCCCCCAACTCTCGGGCATCC 1561
Qy 1441 CAAGATAACGACACCGACTGGGGGTATTGA 1470
Db 1562 CAAGATAACGACACCGACTGGGGGTATTGA 1591

RESULT 7

US-09-951-061A-125
; Sequence 125, Application US/09951061A
; Publication No. US20030082204A1
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Taylor, Jill
; APPLICANT: Gettig, Russell
; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
; TITLE OF INVENTION: RECOMBINANTS
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/951.061A
; FILING DATE: 13-SEP-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/354,138
; FILING DATE: 15-JUL-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,657
; FILING DATE: 16-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,962
; FILING DATE: 08-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/776,867
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,614
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,283
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,614
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,483
; FILING DATE: 12-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/713,967
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07,666,056
; FILING DATE: 07-MAR-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1572 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-951-061A-125

Query Match 7.3%; Score 106.6; DB 10; Length 1572;
Best Local Similarity 46.0%; Pred. No. 1.6e-24;
Matches 361; Conservative 0; Mismatches 424; Indels 0; Gaps 0;
Qy 499 TCTATCCAGGCTCAGGTATGGTCAACGTAGGAGGCCATGACTGCATATGAGACGCA 558
Db 505 TCCATCTTTGGCTCAAATTTGGATCCTGCTAGCTAAAGCGGTACTGCTCTGATATGCA 564
Qy 559 GATGAGTCGGAAACAAAGAGAAATCAATAAGTACATGCGAGGAGGAGGAGTCCAGAGAG 618
Db 565 GCCGACTCGGAGATGAGAGGTGATTAAGTATATCCAGCAAGACGCTGTGGTGGAGAA 624
Qy 619 TACATCTCTCCACCTGTATGCGAGGAGTGCAATCAACTCACAATCAGACATTTCTTGCA 678
Db 625 TTTAGAAATGAACAAAATCTGGCTTGATATTGTTAGAAACAGGATTTGCTGAGGACTATCT 684
Qy 679 GTCCGCAATTTCTTAGTTAGGAGCTTAAAGAGAGGCCGCAATAGCGGAGTGGAGCTCC 738
Db 685 TTGAGGCGATTCATGGTGGCGCTCATCTTGACATCAAAACGATCCCGAGGAAACAAGCCT 744
Qy 739 ACGTATTACAACTTAGTAGGGGATGTAGACTCATACATCAGGAACACGGACTTACTGCA 798
Db 745 AGAATTCGTGAATGATTTGTGATATAGATTAACATACATTTGGAAGTGGGTTAGCTAGT 804
Qy 799 TTCTTCTTACACTCAAATATGGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGC 858
Db 805 TTCACTCTAACTATCAAGTTTGGCATTTGAAACTATGTATCGGCTCTTGGGTTGCATGAG 864
Qy 859 CTCACAGCGCATATCCAAAGATGAAGCAGCTCATGCGTTTATATCGAGTGAAGGAGAA 918
Db 865 TTTTCGGGAGAAATTAACAACTATTGAATCCCTCATGATGCTATATCAACAGATGGGTGA 924
Qy 919 AATGCGCGGTACATGACATTTGCTAGGTGACAGTATCAGATGAGCTTTGCACCGGCTGAG 978
Db 925 ACAGCACCGTACATGGTTATCTTGGAAAACTCTGTTCAAAACAAATTTAGTGCAGGGTCC 984
Qy 979 TATGCAAGCTTTATTTTTCATGGGATGCGCATCAGTCTTTAGATAAAGAACTGGC 1038
Db 985 TACCCATTTGCTCTGGAGTTATGCTATGGGGTTGGTGTGAACTTGAAGAACTCCATGGGA 1044
Qy 1039 AAATACCAATTCGCGAGAGACTTCATGAGCAGATCATTTCTGGAGACTCGGGGTGGAGTAT 1098
Db 1045 GGGTTAAATTTTCGGTCTGATCTTACTTTGACCCAGCTTACTTTCAGACTCGGGCAAGAAATG 1104
Qy 1099 GCTCAGGCTCAGGGGAGTAGCATCAACGAGACATGCTGCTGCTGAGCTTAAACTAACCCCG 1158
Db 1105 GTTAGAGATCTCCCGGCAAGTAAGCTCTGCACTTTCGCGCCGAGCTTGGCATCACCAAG 1164
Qy 1159 GCAGCAAGAGGGGCGCTGGCAGCTGCTGCCAACGAGTGTCTGAGGAAATCTGGCAGCGTG 1218
Db 1165 GAGGAAGCTCAGCTAGTGTGAGAAATAGCATCAAGACACACAGAGACCGGACAAATCGA 1224
Qy 1219 GATATTCCTACTCAACAGCGGGGTCTCTCATCTGGGCTCAGCGATCGAGGCCCGGAGCC 1278
Db 1225 GCTACTGGTCTTAAGCAATCCCAATCACTTTTCTGCACTCGGAAAGATCCGAAAGTCGCC 1284
Qy 1279 TCTCA 1283

; TITLE OF INVENTION: Attenuated Human-Bovine Chimeric Parainfluenza Virus (PIV) Vaccin
; FILE REFERENCE: NIH-0127
; CURRENT APPLICATION NUMBER: US/09/900,112
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/215,809
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 15456
; TYPE: DNA
; ORGANISM: bovine PIV3 Ka strain
US-09-900-112-35

Query Match 5.2%; Score 76; DB 10; Length 15456;
Best Local Similarity 54.7%; Pred. No. 1.5e-13;
Matches 151; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 755 TAGGGGATGTAGACTCATACATCAGGAACACCGGACTTACTGCAATCTTCTTACACTCA 814
DB 868 TACAGATTGTAGGAACACTACATCAGAGATCGAGTCTTGCTTCATTTTCAACAAATCA 927
QY 815 AATATGGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCCTCACAAGCGGATATCC 874
DB 928 GATATGCAATGAGACTAGAGTGGCAGCTCTAACTCTGTCTACCTTAGACCGGATATCA 987
QY 875 AAGAATGAGCAGCTCATCGCTTTATATCGGATGAGGAGGAGAAATGCGCGGTACATGA 934
DB 988 ACAGACTCAAGGCATCATCGAGTTATATCATCAAGGGGCCAGCGTCTCTTTATAT 1047
QY 935 CATTGCTAGTGACAGTGCATGATGAGCTTTCACCGGCTGAGTATGCACAGCTTTATT 994
DB 1048 GCATTTGAGAGATCCGTCGATGAGTTGACCAAGCAACTATCTGCGCCTCTGGA 1107
QY 995 CTTTGGCATGGCATGGCATGCTTATAGATAAG 1030
DB 1108 GTTATGCGATGGTGTAGCAGTTGTACAAAACAAGG 1143

RESULT 10
US-09-900-112-36
; Sequence 36, Application US/09900112
; Publication No. US20030082209A1
; GENERAL INFORMATION:
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Schmidt, Alexander C.
; TITLE OF INVENTION: Attenuated Human-Bovine Chimeric Parainfluenza Virus (PIV) Vaccin
; FILE REFERENCE: NIH-0127
; CURRENT APPLICATION NUMBER: US/09/900,112
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/215,809
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 15456
; TYPE: DNA
; ORGANISM: bovine PIV3 SF strain
US-09-900-112-36

Query Match 5.2%; Score 76; DB 10; Length 15456;
Best Local Similarity 54.7%; Pred. No. 1.5e-13;
Matches 151; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 755 TAGGGGATGTAGACTCATACATCAGGAACACCGGACTTACTGCAATCTTCTTACACTCA 814
DB 868 TACAGATTGTAGGAACACTACATCAGAGATCGAGTCTTGCTTCATTTTCAACAAATCA 927
QY 815 AATATGGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCCTCACAAGCGGATATCC 874
DB 928 GATATGCAATGAGACTAGAGTGGCAGCTCTAACTCTGTCTACCTTAGACCGGATATCA 987

875 ARAAGATGAGCAGCTCATCGCTTTATATCGGATGAGGAGAGAAATGCGCGGTACATGA 934
988 ACAGACTCAAGGCATGATCGAGTTATATCTATCAAGGGGCCACGTCGCTTCTTTTATAT 1047
935 CATTGCTAGTGACAGTGCATGATGAGCTTTCACCGGCTGAGTATGCACAGCTTTATT 994
1048 GCATTTGAGAGATCCGTCGATGAGTTTGACCAAGCAACTATCTGCGCCTCTGGA 1107
995 CTTTGGCATGGCATGGCATGCTTATAGATAAG 1030
1108 GTTATGCGATGGTGTAGCAGTTGTACAAAACAAGG 1143

RESULT 11
US-10-302-547-131
; Sequence 131, Application US/10302547
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADOPOULOS, MARIO H.
; APPLICANT: NEWMAN, JASON T.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE 1 (HPV1) FROM cDNA AND USE OF RECOMBINANT HPV1 IN IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 2303-37-3
; CURRENT APPLICATION NUMBER: US/10/302,547
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/331,961
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 15609
; TYPE: DNA
; ORGANISM: Human parainfluenza virus 1
US-10-302-547-131

Query Match 5.0%; Score 73.2; DB 17; Length 15609;
Best Local Similarity 48.6%; Pred. No. 1.4e-12;
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 762 TGTAGACTCATACATCAGGACACCGGACTTACTGCAATCTTCTTACACTCAATATGG 821
DB 887 TGTAGGAAATTCATAAGAGATCGAGATTAGCATCTTTTCAACACCATCAAGTATGG 946
QY 822 AATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCTCACAAGCGGATATCCAAAAGAT 881
DB 947 TGTAGAAACGAGATGGCCGCTTGACACTATCAATCTGAGACCAGATATAACAATTT 1006
QY 882 GAAGCAGCTCATCGTTTATATCGGATGAAGGAGAGAAATGCGCGGTACATGACTTGGCT 941
DB 1007 GAGAAAGCCTTGTGATATCTATCTATCAAGAGGAGCCGAGCGCCCTTTTATGTAATACT 1066
QY 942 AGTGACAGTGCATGAGCTTTCACCGGCTGAGTATGCACAGCTTTTATTTTTC 1001
DB 1067 CAGAGACCCAGTTTCATGGAGACTTTGCCCCCTGGAACATATCCAGCACTGTGGAGTACGC 1126
QY 1002 CATGGGCGATGGCATCGTCTTAGATAAGGAACTGGCAAAATACCAATTCGCGCAGAGACTT 1061
DB 1127 AATGGGCGTGTGTGTGTAACAAACAAAGCTATGCAACAGTATGTAAGTGAAGACATA 1186
QY 1062 CATGAGCACAATCTTGGAGACTCGGGGTGGAGTATGCTCAGGCTCAGGGGAGTAGCAT 1121
DB 1187 TTTGGACATGGAATGTCTCTACTTGGACAAGCTGTAGCTAAAGATGCTGATTTCCAAAT 1246
QY 1122 CAAGAGACATGGCTGCTGAGCTAAACTAACCCCGGAGCAGAGAGGGGCT 1175
DB 1247 CAGCAGTGTCTTGGAGGAGAACTAGGTGTGACAGATACAGCAAAAGAGAGACT 1300

RESULT 12

US-09-733-692A-60
; Sequence 60, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 15492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pFLC.PIV32, 15492 bp in sense orientation
US-09-733-692A-60

Query Match 4.9%; Score 72.2; DB 9; Length 15492;
Best Local Similarity 54.3%; Pred. No. 3e-12;
Matches 146; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 762 TGTAGACTCATACATCAGAACACCGGACTTACTGCTTCTTCTTACACTCAAAATATGG 821
Db 875 TGTGGCAACTACATAAGAGATGCGGCTCTCGCTTCAATCAATCAGATATGG 934
QY 822 AATTAATACCAAGACATCAGCCCTAGCACTCAGAGGAGAAATCGCGGTACATGACATTGCT 881
Db 935 AATTGAGCCAGAAATGCGAGCTTTGACTCTATCCACTCTCAGACGAGATCAATAGATT 994
QY 882 GAAGCAGCTCATGCGTTTATATCGATGAAGGGAGAAATCGCGGTACATGACATTGCT 941
Db 995 AAAAGCTTTGATGGAACGTATTTATCAAGGGACCGCGCTCTTCTATCTGTATCCT 1054
QY 942 AGGTGACAGTGCATGAGTGGCTTTGACCGGCTGAGTATGCACAGCTTTATCTTTTGC 1001
Db 1055 CAGAGATCTTATACATGCTGAGTTGCGACCGGCAACTATCTCTGCCATATGGAGCTATGC 1114
QY 1002 CATGGGATGGCATCAGCTTCTAGATAAG 1030
Db 1115 AATGGGGTGGCAGTTGTACAAATAGAG 1143

RESULT 13

US-09-733-692A-62
; Sequence 62, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195

; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 15492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pFLC.PIV32CT, 15474 bp in sense orientation
US-09-733-692A-62

Query Match 4.9%; Score 72.2; DB 9; Length 15492;
Best Local Similarity 54.3%; Pred. No. 3e-12;
Matches 146; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 762 TGTAGACTCATACATCAGAACACCGGACTTACTGCTTCTTCTTACACTCAAAATATGG 821
Db 875 TGTGGCAACTACATAAGAGATGCGGCTCTCGCTTCAATCAATCAGATATGG 934
QY 822 AATTAATACCAAGACATCAGCCCTAGCACTCAGAGGAGAAATCGCGGTATCCAAAAGAT 881
Db 935 AATTGAGCCAGAAATGCGAGCTTTGACTCTATCCACTCTCAGACGAGATCAATAGATT 994
QY 882 GAAGCAGCTCATGCGTTTATATCGATGAAGGGAGAAATCGCGGTACATGACATTGCT 941
Db 995 AAAAGCTTTGATGGAACGTATTTATCAAGGGACCGCGCTCTTCTATCTGTATCCT 1054
QY 942 AGGTGACAGTGCATGAGTGGCTTTGACCGGCTGAGTATGCACAGCTTTATCTTTTGC 1001
Db 1055 CAGAGATCTTATACATGCTGAGTTGCGACCGGCAACTATCTCTGCCATATGGAGCTATGC 1114
QY 1002 CATGGGATGGCATCAGCTTCTAGATAAG 1030
Db 1115 AATGGGGTGGCAGTTGTACAAATAGAG 1143

RESULT 14

US-09-733-692A-61
; Sequence 61, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 15498
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pFLC.PIV32TW, 15498 bp in sense orientation
US-09-733-692A-61

Query Match 4.9%; Score 72.2; DB 9; Length 15498;
Best Local Similarity 54.3%; Pred. No. 3e-12;
Matches 146; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 762 TGTAGACTCATACATCAGAACACCGGACTTACTGCTTCTTCTTACACTCAAAATATGG 821
Db 875 TGTGGCAACTACATAAGAGATGCGGCTCTCGCTTCAATCAATCAGATATGG 934
QY 822 AATTAATACCAAGACATCAGCCCTAGCACTCAGAGGAGAAATCGCGGTATCCAAAAGAT 881
Db 935 AATTGAGCCAGAAATGCGAGCTTTGACTCTATCCACTCTCAGACGAGATCAATAGATT 994
QY 882 GAAGCAGCTCATGCGTTTATATCGATGAAGGGAGAAATCGCGGTACATGACATTGCT 941
Db 995 AAAAGCTTTGATGGAACGTATTTATCAAGGGACCGCGCTCTTCTATCTGTATCCT 1054
QY 942 AGGTGACAGTGCATGAGTGGCTTTGACCGGCTGAGTATGCACAGCTTTATCTTTTGC 1001
Db 1055 CAGAGATCTTATACATGCTGAGTTGCGACCGGCAACTATCTCTGCCATATGGAGCTATGC 1114
QY 1002 CATGGGATGGCATCAGCTTCTAGATAAG 1030
Db 1115 AATGGGGTGGCAGTTGTACAAATAGAG 1143


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Db      875 TGTGGCACTACATAAGAGATGAGGTCTCGCTTCATTCTTCAATACATCAGATATGG 934
Qy      822 AATTAAATACCAAGACATCAGCCCTAGCACTCAGCAGCCTCAAGCGGATATCCAAAAGAT 881
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      935 AATTGAGACCAAGATGGCAGCTTTGACTCTATCCACTCTCAGACCAAGATATCAATAGATT 994
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      882 GAAGCAGCTCATGCGTTTATATCGATCAAGGGAGAAATGCGCGGTACATGACATTGCT 941
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      995 AAAAGCTTTGATGGAACGTGTATTTATCAAGGGACCAAGCGCTCCTTTCACTGTATCCT 1054
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      942 AGGTGACAGTGCATGATGAGCTTTTGACCCGCTGAGTATGCACAGCTTTATTTCTTTTGC 1001
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1055 CAGAGATCCTATACATGCTGAGTTGCGACCAAGGCAACTATCCTGCCATATGGAGCTATGC 1114
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1002 CATGGGCATGCGATCAGCTTTAGATAAAG 1030
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1115 AATGGGGTGGCAGTTGTACAAAATAGAG 1143
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RESULT 15

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US-09-764-891-10172
; Sequence 10172, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10172
; LENGTH: 11809
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-10172
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Query Match      2.7%; Score 39.8; DB 10; Length 11809;
Best Local Similarity 60.7%; Pred. No. 0.25;
Matches 65; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy      1333 ACCCAATTTCTTGGATTTGATGAGCGAGTGGGGAACAGCATGCGAGAGCGCCAACTCC 1392
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5643 ATCCAGTCAGGGAGATCCTGAGGATGGGAGCGGACAGACTGGAACTCCAGGCTCCAGGAGG 5702
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Qy      1393 GCACAGAGCACACCCACCCGGAACCCCCCGGACTCCCGGGGCCATC 1439
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Job time : 1004 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 19:36:35 ; Search time 5764 Seconds
(without alignment)
7615.789 Million cell updates/sec

Title: US-09-970-851-1
Perfect score: 1470
Sequence: 1 atgtcttcctgattcgatga.....acacgactgggggtattga 1470

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	48	3.3	910	29	CNS0060N
C 2	46.4	3.2	1201	13	BX356664
C 3	41.6	2.8	1201	13	BX442599
C 4	41.4	2.8	839	29	CNS004NB
C 1	48	3.3	910	29	CNS0060N
C 2	46.4	3.2	1201	13	BX356664
C 3	41.6	2.8	1201	13	BX442599
C 4	41.4	2.8	839	29	CNS004NB

C 5	41.2	2.8	1201	13	BX381961
C 6	41	2.8	452	10	BB785240
C 7	40.6	2.8	940	28	CC421824
C 8	40.2	2.7	475	9	AL450622
C 9	40.2	2.7	835	13	BX468739
C 10	39.6	2.7	486	9	AI917768
C 11	39.6	2.7	1201	13	BX360624
C 12	39.6	2.7	1208	29	AG115851
C 13	39.4	2.7	895	10	BE571023
C 14	39.4	2.7	988	29	CNS0079R
C 15	39.4	2.7	1201	13	BX406481
C 16	38.8	2.6	849	13	BX462111
C 17	38.8	2.6	885	13	BX425603
C 18	38.6	2.6	298	10	BB026608
C 19	38.4	2.6	600	12	B1813308
C 20	38.4	2.6	1101	29	CNS00F3N
C 21	38.2	2.6	344	14	CF244892
C 22	38.2	2.6	975	29	CC837496
C 23	38.2	2.6	1042	28	CC246998
C 24	38	2.6	1260	13	BQ677411
C 25	37.8	2.6	1101	29	CNS016HG
C 26	37.6	2.6	459	29	CE329457
C 27	37.6	2.6	991	28	CC241937
C 28	37.4	2.5	419	9	AI009304
C 29	37.2	2.5	494	14	CE713434
C 30	37.2	2.5	551	14	CD660629
C 31	37.2	2.5	640	14	CD466270
C 32	37.2	2.5	651	14	CD535076
C 33	37.2	2.5	828	29	CNS048X6
C 34	37.2	2.5	993	13	BX400687
C 35	37.2	2.5	1064	29	CNS020AS
C 36	37	2.5	454	14	CD407576
C 37	37	2.5	510	12	BG905028
C 38	36.8	2.5	435	12	B1437139
C 39	36.8	2.5	633	13	BU546640
C 40	36.8	2.5	682	28	AQ656834
C 41	36.8	2.5	716	28	BH519387
C 42	36.8	2.5	1201	13	BX401671
C 43	36.8	2.5	1287	10	BF664989
C 44	36.8	2.5	2319	13	BUL99108
C 45	36.8	2.5	3183	11	BC034944

ALIGNMENTS

RESULT 1
CNS0060N/c

LOCUS

DEFINITION

CNS0060N 910 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL065629
GI:4944698
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 910)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org/TheBDGP/Drosophila>
melanogaster BAC library was prepared by Kazutoyo Ooeagawa and
Aaron Mammoseer in Pieter de Jong's laboratory in the Department of


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/db_xref="taxon:9606"
/clone="CS0DF033YP22"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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Query Match 2.8%; Score 41.6; DB 13; Length 1201;
Best Local Similarity 35.9%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 97; Conservative 40; Mismatches 133; Indels 0; Gaps 0;

ORIGIN

1111 GCGAGTAGCATCAACGAAGACATGGCTGTGAGCTAAACTAACCCCGGAGCAAGAGG 1170
Db SGGANAMCCGKDCSCSACCCRMCCGGAAGARGAARACCAKCGKCGKMAWMC 1007
1171 GGCCTGGAGCTGTCGCCAAGAGTGTCTGAGGAACTGGCAGCGTGATATTCCTACT 1230
Db SXCDAKCTGGKGTCCMAAAAGACYGKGTGAACCCSKAAACMSKGRITSMCCCCCCC 947
1231 CAACAGCGGGTCTCACTGGCTCAGCGATGGAGGCCCGCGCTCTCAGGTTGA 1290
Db CRCCCGGGGGYCCCGCAGAGGTGACCCSCAAGGAGWGTGAGAMGAGGRCMAAGC 887
1291 TCGAACAACTGCGAAGGGCAACAGATGCGGAGATGGGAGACCCAAATCTTGGATTG 1350
Db CAGAAAAGGGAGGGGGCCMCWAGCCGCGACSCGCGGTCCCGCAAKCAKACMAG 827
1351 ATGAGAGCAGTGGCGAACAGCATGCGAGAA 1380
Db AGGAGKNCACAAAGGAGAGRRGTGGAGAA 797

RESULT 4

CNS004NB 839 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR10E16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL054280
VERSION AL054280.1 GI:4931788
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 839)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers

FEATURES

source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YF05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V

source

1. .839
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR10E16"
/clone_lib="RPCI-98"
/note="end : TET3"

Query Match 2.8%; Score 41.4; DB 29; Length 839;
Best Local Similarity 19.5%; Pred. No. 1.7;
Matches 60; Conservative 113; Mismatches 134; Indels 0; Gaps 0;

ORIGIN

1128 AGCATGGCTGTGAGCTAAACTAACCCCGGAGCAAGAGGCTGTGAGCTGTCTGC 1187
Db ASASGGCSASSCAACSSACAGSAGSSASGSCAGSSSSAGGSGSAGSSGSG 533
1188 CCAACAGTGTCTGAGGAACTGGCAGCGTGATATTCCTACTCAACAAAGCCGGTCT 1247
Db GAGSGSGGGSGRSGCGGAVGSAGSSSACSCSASSSSSSSSASGCMSCSSSSSAA 593
1248 CACTGGGCTCAGGATGGAGGCCCGCGAGCTCTCAGGTTGATCGAACAGTCCGCAAG 1307
Db SCSSSSSSGSAVAACVCSGSGSGVGSAAAVARSGARGMGMAAGSGRAVSAASAAAS 653
1308 GCAACAGATGCGGAGATGGGAGACCCAAATCTTGGATTCTGATGAGCAGTGGCGAA 1367
Db ASAAAVGAAACSSGSGAGSSAGAAARACASVCASSSSGSCGSSSMCSAVSGAA 713
1368 CAGCATGCGAGAGCGCCAACTCCGACAGAGCACACCCACCCGGAACCCCCCGGAC 1427
Db SSGASGCGCGSSSGSCSCSCSSSSSSGCGSVCSGSSVCSGSSVCSGSSSBBSSC 773
1428 TCCCGG 1434
Db 774 SCCASS 780

RESULT 5

BX381961/c 1201 bp mRNA linear EST 08-MAY-2003
LOCUS BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1072YF05 3-PRIME, mRNA sequence.

ACCESSION BX381961
VERSION BX381961.1 GI:30453007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1072CC03NP1.
Location/Qualifiers

FEATURES

source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YF05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V


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Class: sheared ends.
FEATURES
  source
    Location/Qualifiers
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        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
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        /clone_lib="ZM 0.6-1.0 kb"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
        Cor selected genomic DNA library"
ORIGIN
  Query Match          2.8%; Score 40.6; DB 28; Length 940;
  Best Local Similarity 53.8%; Pred. No. 3.2; Mismatches 89; Indels 1; Gaps 1;
  Matches 105; Conservative 0;
  QY 685 ATTTCTTTAGTACGAGCTTAAGAGAGCGCCCAATACGGCAGGTGGGAGCTCCACGTAT 744
  Db 223 ATACTATTTTCAAGGAACCTAAGAGAGAAAATAAATAAAGTAGAAAAATAATAC 164
  QY 745 TACAACCTAGTAGGGATGTAGACTATACATCAGGAACACCGGACTTACTGCAATCTTC 804
  Db 163 AATAA-TTCCAAATGAATGTAAACAACATCTATTGGAAGAGATGAATGATTGAATTTCTT 105
  QY 805 CTTACACTCAATATGGAATTAATACCAAGACATCAGCCCTAGCACTCAGCAGCTTACA 864
  Db 104 GATCATTAAGAAGAGGTATAGTTTCAAAACATCAGTCATCCAGTCAGAGTTCTCAAG 45
  QY 865 GGCATATCCAAAAG 879
  Db 44 GGAACACCCAAAAG 30

RESULT 8
AL450622
LOCUS AL450622 Hordeum vulgare Barke etiolated leaves Hordeum vulgare
DEFINITION subsp. vulgare cDNA clone HK03H20u 5', mRNA sequence.
ACCESSION AL450622
VERSION AL450622.1 GI:11602030
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 475)
  Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
  EST sequencing and analysis in barley
  Unpublished (2000)
  Contact: Michalek W
  Institute for Plant Genetics and Crop Plant Research
  Corrensstr.3, D-06466 Gatersleben, Germany
  Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
  Seq primer: M13uni primer for 5'end.
FEATURES
  source
    Location/Qualifiers
      1..475
        /organism="Hordeum vulgare subsp. vulgare"
        /mol_type="mRNA"
        /cultiivar="barke"
        /sub_species="vulgare"
        /db_xref="taxon:112509"
        /clone="HK03H20u"
        /tissue_type="etiolated leaves"
        /lab_host="XliBlue"
        /clone_lib="Hordeum vulgare Barke etiolated leaves"
        /note="Vector: pluescript SK; Site 1: SalI; Site 2:
        NciI; mRNA was made from etiolated leaves of spring barley
        variety 'Barke', a high quality malting variety. Plants
        were grown on filterpaper for 6 d at 25 C in the dark.
        Leaves were harvested at daylight conditions. Sal-Adaptor
        Sequence: TCGACCCACGCTCG Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'- and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp."
ORIGIN
  Query Match          2.7%; Score 40.2; DB 9; Length 475;
  Best Local Similarity 55.3%; Pred. No. 2.8;
  Matches 78; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
  QY 1241 GGGTCTCTCACTGGGCTCAGCGATGAGGCGCCCGAGCCTCTCAGGTTGGATCGAACAGT 1300
  Db 74 GGTTCGAGCTCTGTCCGACATGCGCTGCGCTCCGCTCAAGTGTGACCGGAGGCG 133
  QY 1301 CGCAAGGCAACACAGATCCGGAGATGGGAGAGACCCAAATTTCTTGATTTGATGAGAGCAG 1360
  Db 134 GGCAACTTCGTGGAGGCGCGGAGCTGGAGCGGCGGTGAGTGCTCTGATGGCGGAGGAG 193
  QY 1361 TGGCGACAGCATGCGAGAAG 1381
  Db 194 GGGAGGACGGCCAGGGAGAAG 214

RESULT 9
BX468739
LOCUS BX468739 NAP1 Anopheles gambiae cDNA clone NAP1-P138-H-07-5, mRNA
DEFINITION sequence.
ACCESSION BX468739
VERSION BX468739.1 GI:31659680
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
1 (bases 1 to 835)
  Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.
  and Kafatos,F.C.
  Anopheles gambiae EST, European Molecular Biology Laboratory
  Unpublished (2002)
  Contact: Christophides GK
  Foris C. Kafatos laboratory
  European Molecular Biology Laboratory
  Meyerhofstrasse 1, 69117 Heidelberg, Germany
  Tel: +49 6221 387-440
  Fax: +49 6221 387-306
  Email: christop@embl-heidelberg.de
  Contact: Christophides G.K.
  European Molecular Biology Laboratory
  Meyerhofstr. 1, 69117 Heidelberg, Germany.
  Tel: +49 6221 387- 440
  Fax: +49 6221 387-306
  Email: christop@embl-heidelberg.de
  Plate: P138 row: H column: 07.
FEATURES
  source
    Location/Qualifiers
      1..835
        /organism="Anopheles gambiae"
        /mol_type="mRNA"
        /db_xref="taxon:7165"
        /clone="NAP1-P138-H-07-5"
        /lab_host="E. coli DH10B"
        /clone_lib="NAP1"
        /note="Vector: pT73D-Pac (Pharmacia); Site 1: NotI;
        Site 2: EcoRI; ESTs sequenced from the T7 priming site
        that reads from the 5' end of cDNA. The NAP1 is a
        directionally cloned and normalized, oligo-T primed cDNA
        library constructed from a mixture of Anopheles gambiae
        developmental stages according to: Bonaldo, Lennon &
        Soares (1996): Normalization and Subtraction: Two
        Approaches To Facilitate Gene Discovery, Genome Research
        6, 791-806."
ORIGIN

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Query Match 2.7%; Score 40.2; DB 13; Length 835;
 Best Local Similarity 54.4%; Pred. No. 3.9;
 Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 291 TACACTGACTGTTCTTGGATCGATGGTGTATTTACACAGCGCGTCTCAGTTTCAACAACAG 350
 DB 180 TAACTCGATGTAATGATATCGAGTGTGGCTGTCCCGTGTCCAGTTTCCAGTTTCCAAAC 239

QY 351 GAGTGGGTGTTCTGAGGAGAGACACAGATTCATGATGATGATGATGATGATGATGATGATG 410
 DB 240 GGGGGGAATTTGTTTGAATGTTGACAGAAATGCTTTAATGCGGAAGGCGGAGAGCCGG 299

QY 411 GCGGTGCACTAACGGTACTCCGTTCTGTCA 439
 DB 300 CTGGGAATTTACGGGACAACGTTGGTTA 328

RESULT 10
 AI917768/c
 LOCUS AI917768 486 bp mRNA linear EST 17-DEC-1999
 DEFINITION wbl5904.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305782 3',
 mRNA sequence.
 ACCESSION AI917768
 VERSION AI917768
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 486)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1052 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 462.

FEATURES
 source
 1..486
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2305782"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP GC6"
 /notes="Vector: pTV73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI_CGAP GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 2.7%; Score 39.6; DB 9; Length 486;
 Best Local Similarity 47.9%; Pred. No. 4.3;
 Matches 114; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 248 TGATGAGGAACCATGTTGCTTTCAGGAAACAGATGAGGCTACACTGTTCTTG 307
 DB 391 TGTGAGGAACCAATGTTGCTTTCCTGTCATCAACAGCCACCTCTCTTCTCTAA 322

QY 308 AGATCGATGTTTACACAGCGTGTCTCAGTTTCAACAACAGGAGTGGGTGCTGAGG 367
 DB 321 ATGATCTGGCTTTTCTCTGGAGGCTGCCATGTTTGAAGATGGTATCAGAGGGCTGCT 262

QY 368 AGAGACACAGAGATTCATGTTGATGACAGGCTCTCTCCCTCGGCGTGCAGTAACGGTA 427
 DB 261 GGGCAGTCTGCTTCGGGCGCAGGCTCAGGACCCCTCTGCTCTGACGCTTAACTGTC 202

QY 428 CTCCGTTGCTCACGCTGGGTTGAAGATGATGACACCAAGATATCACTGATCTCT 485
 DB 201 CTCTGCTAGGACCGGTTGATTTCAAGCCAGGAAGCAACTGGGACCCCTGAAAACTGT 144

RESULT 11
 BX360624
 LOCUS BX360624 1201 bp mRNA linear EST 05-MAY-2003
 DEFINITION clone CS0DI072YL05 3-PRIME, mRNA sequence.
 ACCESSION BX360624
 VERSION BX360624.1 GI:30376452
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4982.r
 Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI072CF03NP1.

FEATURES
 source
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI072YL05"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 2.7%; Score 39.6; DB 13; Length 1201;
 Best Local Similarity 11.6%; Pred. No. 7.4;
 Matches 34; Conservative 152; Mismatches 105; Indels 1; Gaps 1;

QY 1173 CTGTGAGCTGTGCTCCCAACGAGTGTCTGAGGAACTGCGAGGTGATTCCTACTCA 1232
 DB 904 SSSSSSSSTAGSWMNSASS 963

QY 1233 ACAAGCGGGTCTCTACTGGGCTACGCGTACGAGGCCCCCGAGGCTCTCAGGGTGCATC 1292
 DB 964 SSS 1023

QY 1293 GAACAGTCGCAAGGCAACACGATCCCGAGATGGGAGACCAATCTTCTGGATTGAT 1352
 DB 1024 SVSVVASSRAASS 1083

QY 1353 GAGAGCAGTGGCGAACAGCATGCGGAAGCGCCAACTCGGCACAGACCAACCCACC 1412

RESULT 13					
BE571023					
LOCUS	BE571023	895 bp	mRNA	linear	EST 15-AUG-2000
DEFINITION	601334530F1 NCI CGAP Mam6 Mus musculus cDNA clone IMAGE:3711894 5', mRNA sequence.				

VERSION	BE571023.1	GI:9814743
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 895)	
TITLE	NIH-MGC http://mgc.nci.nih.gov/	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	

REFERENCE	1 (bases 1 to 895)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM8936 row: 1 column: 07
 High quality sequence start: 6
 High quality sequence stop: 362.

FEATURES	source
Location/Qualifiers	
1. .895	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="FVB/N"	
/db_xref="taxon:10090"	
/clone="IMAGE:3711894"	
/sex="female, virgin"	
/tissue type="infiltrating ductal carcinoma"	
/dev_stage="5 months"	
/lab_host="DH10B"	
/clone_lib="NCI CGAP Mam6"	
/note="mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dm."	
Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"	

ORIGIN	Query Match	2.7%;	Score 39.4;	DB 10;	Length 895;
	Best Local Similarity	52.1%;	Pred. No. 7.1;		
	Matches 112;	Conservative 0;	Mismatches 101;	Indels 2;	Gaps 1;
QY	1050	CGCCAGAGACTTCATGAGCACATCATCTCGGAGACTCGGGGTGAGGTATGCTCAGGCTCA	1109		
Db	647				
		CGCCCGAGGATAAATCTGAACGTAAATCTCCAGACTGACGGATCTGTTGTATGGAATAA	706		
QY	1110	GGGGAGTAGCATCAACGAAGACATGCGCTGCTGAG--CTAAACTAATACCCGGCAGCAAGA	1167		
Db	707	GGGGCCCTAACCCCTCTGTGTGATCTGGGAGATGTGGCCAATCAGTGCGCCGACAAGGTACA	766		
QY	1168	AGGGGCTCGCAGCTCTGCCCAACGAGTGTCTGAGAAACTGGCGACGCTGGATATTCCT	1227		
Db	767	AGGRCAGGGGACCTGGTTCTTCGACGGGGGAACCTGGGAACCATATACGGGGTGCAAACT	826		
QY	1228	ACTCAACAAGCGGGGTCTCTCACTGGGCTCAGCGA	1262		
Db	827	CGGAACACGAGGGGGCTATCACAGGGCCCTGAGA	861		

RESULT 14	LOCUS	CNS0079R	988 bp	DNA	linear	GSS 03-JUN-1999
		Drosophila melanogaster genome survey sequence T7 end of BAC #				
		BACR15G10 of RPC1-98 library from Drosophila melanogaster (fruit				
	DEFINITION					

